



SEQUENCE LISTING

<110> PANGALOS, MENLAS
NEEFS, JEAN-MARC, EDMOND, FERNAND, MARIE
PEETERS, DANIELLE, CELINE, GEORGETTE

<120> CLONING AND CHARACTERISATION OF NOVEL MAMMALIAN
PEPTIDASES

<130> JAB1407US

<140> 09/743,647
<141> 2001-01-12

<150> PCT/GB99/02241
<151> 1999-07-14

<150> GB 9815284.6
<151> 1998-07-14

<160> 69

<170> PatentIn Ver. 3.3

<210> 1
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primer

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<210> 2
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primer

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primer

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primer

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<210> 11
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 <210> 15
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primer

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<210> 33
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<400> 33
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<210> 34
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Met Gln Trp Thr Lys Val Leu Gly Leu Gly Leu Gly																		
1						5						10						
gct	gct	gcc	ctc	ttg	ggg	ctg	ggg	atc	atc	ctc	ggc	cac	ttt	gcc	atc		100	
Ala	Ala	Ala	Leu	Leu	Gly	Leu	Gly	Ile	Ile	Leu	Gly	His	Phe	Ala	Ile			
15						20			25									
ccc	aaa	aaa	gcc	aac	tca	ctg	gcc	ccc	cag	gac	ctg	gac	ctg	gag	atc		148	
Pro	Lys	Lys	Ala	Asn	Ser	Leu	Ala	Pro	Gln	Asp	Leu	Asp	Leu	Glu	Ile			
30						35			40									
ctg	gag	acc	gtc	atg	ggg	cag	ctg	gat	gcc	cac	agg	atc	cgg	gag	aac		196	
Leu	Glu	Thr	Val	Met	Gly	Gln	Leu	Asp	Ala	His	Arg	Ile	Arg	Glu	Asn			
45			50						55			60						
ctc	aga	gaa	ctc	tcc	agg	gag	cca	cac	ctg	gcc	tcc	agc	cct	cgg	gat		244	
Leu	Arg	Glu	Leu	Ser	Arg	Glu	Pro	His	Leu	Ala	Ser	Ser	Pro	Arg	Asp			
			65						70			75						
gag	gac	ctg	gtg	cag	ctg	ctg	ctg	cag	cgc	tgg	aag	gac	cca	gag	tca		292	
Glu	Asp	Leu	Val	Gln	Leu	Leu	Leu	Gln	Arg	Trp	Lys	Asp	Pro	Glu	Ser			
80						85						90						
ggc	ctg	gac	tcg	gcc	gag	gcc	tnc	acg	tac	gaa	gtg	ctg	ctg	tcc	ttc		340	
Gly	Leu	Asp	Ser	Ala	Glu	Ala	Xaa	Thr	Tyr	Glu	Val	Leu	Leu	Ser	Phe			
95						100						105						
cct	agc	cag	gag	cag	ccc	aac	gtc	gtg	gac	atc	gtg	ggc	ccc	act	ggg		388	
Pro	Ser	Gln	Glu	Gln	Pro	Asn	Val	Val	Asp	Ile	Val	Gly	Pro	Thr	Gly			
110						115			120									
ggc	atc	atc	cac	tcc	tgc	cac	cgg	act	gag	gag	aac	gtg	acc	ggg	gag		436	
Gly	Ile	Ile	His	Ser	Cys	His	Arg	Thr	Glu	Glu	Asn	Val	Thr	Gly	Glu			
125			130						135			140						
caa	ggg	ggg	cca	gat	gtg	gta	caa	ccc	tat	gct	gcc	tat	gct	cct	tct		484	
Gln	Gly	Gly	Pro	Asp	Val	Val	Gln	Pro	Tyr	Ala	Ala	Tyr	Ala	Pro	Ser			
			145						150			155						
gga	acc	cca	cag	ggc	ctc	ctc	gtc	tat	gcc	aac	cgg	ggc	gcg	gaa	gaa		532	
Gly	Thr	Pro	Gln	Gly	Leu	Leu	Val	Tyr	Ala	Asn	Arg	Gly	Ala	Glu	Glu			
			160			165						170						
gac	ttt	aag	gag	cta	cag	act	cag	ggc	atc	aaa	ctt	gaa	ggc	acc	att		580	
Asp	Phe	Lys	Glu	Leu	Gln	Thr	Gln	Gly	Ile	Lys	Leu	Glu	Gly	Thr	Ile			
175						180						185						

gcc ctg act cga tat ggg ggt gta ggg cgt ggg gcc aag gct gtg aac	628
Ala Leu Thr Arg Tyr Gly Gly Val Gly Arg Gly Ala Lys Ala Val Asn	
190 195 200	
gct gcc aag cac ggg gta gct ggg gtg ctg gtg tac aca gac cct gcc	676
Ala Ala Lys His Gly Val Ala Gly Val Leu Val Tyr Thr Asp Pro Ala	
205 210 215 220	
gac atc aac gat ggg ctg agc tca ccc gac gaa acc ttt ccc aac tcc	724
Asp Ile Asn Asp Gly Leu Ser Ser Pro Asp Glu Thr Phe Pro Asn Ser	
225 230 235	
tgg tac ctg ccc ccc tca gga gtg gag cga ggc tcc tac tac gag tat	772
Trp Tyr Leu Pro Pro Ser Gly Val Glu Arg Gly Ser Tyr Tyr Glu Tyr	
240 245 250	
ttt ggg gac cct ctg act ccc tac ctt cca gcc gtc ccc tct tcc ttc	820
Phe Gly Asp Pro Leu Thr Pro Tyr Leu Pro Ala Val Pro Ser Ser Phe	
255 260 265	
cgc gtg gac ctt gcc aat gtc tcc gga ttt ccc cca att cct aca cag	868
Arg Val Asp Leu Ala Asn Val Ser Gly Phe Pro Pro Ile Pro Thr Gln	
270 275 280	
ccc att ggc ttc cag gat gca aga gac ctg ctc tgt aac ctc aac gga	916
Pro Ile Gly Phe Gln Asp Ala Arg Asp Leu Leu Cys Asn Leu Asn Gly	
285 290 295 300	
act ttg gcc cca gcc acc tgg cag gga gca ctg ggc tgc cac tac agg	964
Thr Leu Ala Pro Ala Thr Trp Gln Gly Ala Leu Gly Cys His Tyr Arg	
305 310 315	
ttg ggt ccc ggc ttc cgg cct gac gga gac ttc cca gca gac agc cag	1012
Leu Gly Pro Gly Phe Arg Pro Asp Gly Asp Phe Pro Ala Asp Ser Gln	
320 325 330	
gtg aat gtg agc gtc tac aac cgc ctg gag ctg agg aac tct tcc aac	1060
Val Asn Val Ser Val Tyr Asn Arg Leu Glu Leu Arg Asn Ser Ser Asn	
335 340 345	
gtc ctg ggc atc atc cgt ggg gct gtg gag cct gat cgc tac gtg ctg	1108
Val Leu Gly Ile Ile Arg Gly Ala Val Glu Pro Asp Arg Tyr Val Leu	
350 355 360	
tat ggg aac cac cga gac agc tgg gtg cac ggg gct gtg gac ccc agc	1156
Tyr Gly Asn His Arg Asp Ser Trp Val His Gly Ala Val Asp Pro Ser	
365 370 375 380	
agt ggc acc gcc gtc ctc ctg gag ctc tcc cgt gtc ctg ggg acc ctg	1204
Ser Gly Thr Ala Val Leu Leu Glu Leu Ser Arg Val Leu Gly Thr Leu	
385 390 395	
ctg aag aag ggc acc tgg cgt cct cgc aga tca atc gtg ttt gcg agc	1252
Leu Lys Lys Gly Thr Trp Arg Pro Arg Arg Ser Ile Val Phe Ala Ser	
400 405 410	

tgg ggg gct gag gag ttt ggg ctc att ggc tcc acg gaa ttc aca gaa	1300
Trp Gly Ala Glu Glu Phe Gly Leu Ile Gly Ser Thr Glu Phe Thr Glu	
415 420 425	
 gag ttc ttc aac aag ctg cag gag cgc acg gtg gcc tac atc aac gtg	1348
Glu Phe Phe Asn Lys Leu Gln Glu Arg Thr Val Ala Tyr Ile Asn Val	
430 435 440	
 gac atc tcg gtg ttt gcc aac gct acc ctt agg gtg cag ggg acg ccc	1396
Asp Ile Ser Val Phe Ala Asn Ala Thr Leu Arg Val Gln Gly Thr Pro	
445 450 455 460	
 cct gtc cag agc gtc gtc ttc tct gca acc aaa gag atc cgc tca cca	1444
Pro Val Gln Ser Val Val Phe Ser Ala Thr Lys Glu Ile Arg Ser Pro	
465 470 475	
 ggc cct ggc gac ctg agc atc tac gac aac tgg atc cgg tac ttc aac	1492
Gly Pro Gly Asp Leu Ser Ile Tyr Asp Asn Trp Ile Arg Tyr Phe Asn	
480 485 490	
 cgc agc agc ccg gtg tac ggc ctg gtc ccc agc ttg ggt tct ctg ggt	1540
Arg Ser Ser Pro Val Tyr Gly Leu Val Pro Ser Leu Gly Ser Leu Gly	
495 500 505	
 gct ggc agc gac tat gca ccc ttc gtt cac ttc ctg ggc atc tcc tcc	1588
Ala Gly Ser Asp Tyr Ala Pro Phe Val His Phe Leu Gly Ile Ser Ser	
510 515 520	
 atg gac att gcc tat acc tat gac cgg agc aag act tca gcc agg atc	1636
Met Asp Ile Ala Tyr Thr Tyr Asp Arg Ser Lys Thr Ser Ala Arg Ile	
525 530 535 540	
 tac ccc acc tac cac aca gcc ttt gac acc ttt gac tat gtg gac aag	1684
Tyr Pro Thr Tyr His Thr Ala Phe Asp Thr Phe Asp Tyr Val Asp Lys	
545 550 555	
 ttt ttg gac ccg ggc ttc agc agc cat cag gct gtg gcc cgg aca gcg	1732
Phe Leu Asp Pro Gly Phe Ser Ser His Gln Ala Val Ala Arg Thr Ala	
560 565 570	
 ggg agt gtg att ctc cgg ctc agt gac agc ttc ttc ctg ccc ctc aaa	1780
Gly Ser Val Ile Leu Arg Leu Ser Asp Ser Phe Phe Leu Pro Leu Lys	
575 580 585	
 gtc agt gac tac agt gag aca ctc cgc agc ttc ctg cag gca gcc cag	1828
Val Ser Asp Tyr Ser Glu Thr Leu Arg Ser Phe Leu Gln Ala Ala Gln	
590 595 600	
 caa gat ctt ggg gcc ctg ctg gag cag cac agc atc agc ctg ggg cct	1876
Gln Asp Leu Gly Ala Leu Leu Glu Gln His Ser Ile Ser Leu Gly Pro	
605 610 615 620	
 ctg gtg act gca gtg gag aag ttt gag gca gaa gct gca gcc ttg ggc	1924
Leu Val Thr Ala Val Glu Lys Phe Glu Ala Glu Ala Ala Leu Gly	
625 630 635	

caa cgc ata tca aca ctg cag aag ggc agc cct gac ccc ctg cag gtc 1972
 Gln Arg Ile Ser Thr Leu Gln Lys Gly Ser Pro Asp Pro Leu Gln Val
 640 645 650

 cgg atg ctc aat gac cag ttg atg ctc ttg gaa cgg acc ttt ctg aac 2020
 Arg Met Leu Asn Asp Gln Leu Met Leu Leu Glu Arg Thr Phe Leu Asn
 655 660 665

 cct aga gcc ttc cca gag gaa cgc tac tac agc cat gtg ctc tgg gca 2068
 Pro Arg Ala Phe Pro Glu Glu Arg Tyr Tyr Ser His Val Leu Trp Ala
 670 675 680

 cct tcg cac ggg ctc cgt agt cac att ccg ggg cta tcc aat gcc tgc 2116
 Pro Ser His Gly Leu Arg Ser His Ile Pro Gly Leu Ser Asn Ala Cys
 685 690 695 700

 tcc agg gcc agg gac aca gct tct gga tct gaa gct tgg gct gag gtc 2164
 Ser Arg Ala Arg Asp Thr Ala Ser Gly Ser Glu Ala Trp Ala Glu Val
 705 710 715

 cag aga cag ctc agc att gtg gtg aca gcc ctg gag ggt gcg gca gcc 2212
 Gln Arg Gln Leu Ser Ile Val Val Thr Ala Leu Glu Gly Ala Ala Ala
 720 725 730

 acc ctg agg cct gtg gct gac ctc tgacccccagc cctcttttctt cagccctccc 2266
 Thr Leu Arg Pro Val Ala Asp Leu
 735 740

 ttctactccgg tgcttttatat ttacaaagtg ctttgtgttt tttaaaagtc tttt 2320

<210> 35

<211> 740

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (100)

<223> variable amino acid

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Met Gln Trp Thr Lys Val Leu Gly Leu Gly Leu Gly Ala Ala Ala Leu
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Leu Gly Leu Gly Ile Ile Leu Gly His Phe Ala Ile Pro Lys Lys Ala
 20 25 30

Asn Ser Leu Ala Pro Gln Asp Leu Asp Leu Glu Ile Leu Glu Thr Val
 35 40 45

Met Gly Gln Leu Asp Ala His Arg Ile Arg Glu Asn Leu Arg Glu Leu
 50 55 60

Ser Arg Glu Pro His Leu Ala Ser Ser Pro Arg Asp Glu Asp Leu Val
 65 70 75 80

Gln	Leu	Leu	Leu	Gln	Arg	Trp	Lys	Asp	Pro	Glu	Ser	Gly	Leu	Asp	Ser	
				85					90					95		
Ala	Glu	Ala	Xaa	Thr	Tyr	Glu	Val	Leu	Leu	Ser	Phe	Pro	Ser	Gln	Glu	
				100					105					110		
Gln	Pro	Asn	Val	Val	Asp	Ile	Val	Gly	Pro	Thr	Gly	Gly	Ile	Ile	His	
				115					120					125		
Ser	Cys	His	Arg	Thr	Glu	Glu	Asn	Val	Thr	Gly	Glu	Gln	Gly	Gly	Pro	
				130					135					140		
Asp	Val	Val	Gln	Pro	Tyr	Ala	Ala	Tyr	Ala	Pro	Ser	Gly	Thr	Pro	Gln	
				145					150					155		
Gly	Leu	Leu	Val	Tyr	Ala	Asn	Arg	Gly	Ala	Glu	Glu	Asp	Phe	Lys	Glu	
				165					170					175		
Leu	Gln	Thr	Gln	Gly	Ile	Lys	Leu	Glu	Gly	Thr	Ile	Ala	Leu	Thr	Arg	
				180					185					190		
Tyr	Gly	Gly	Val	Gly	Arg	Gly	Ala	Lys	Ala	Val	Asn	Ala	Ala	Lys	His	
				195					200					205		
Gly	Val	Ala	Gly	Val	Leu	Val	Tyr	Thr	Asp	Pro	Ala	Asp	Ile	Asn	Asp	
				210					215					220		
Gly	Leu	Ser	Ser	Pro	Asp	Glu	Thr	Phe	Pro	Asn	Ser	Trp	Tyr	Leu	Pro	
				225					230					235		
Pro	Ser	Gly	Val	Glu	Arg	Gly	Ser	Tyr	Tyr	Glu	Tyr	Phe	Gly	Asp	Pro	
				245					250					255		
Leu	Thr	Pro	Tyr	Leu	Pro	Ala	Val	Pro	Ser	Ser	Phe	Arg	Val	Asp	Leu	
				260					265					270		
Ala	Asn	Val	Ser	Gly	Phe	Pro	Pro	Ile	Pro	Thr	Gln	Pro	Ile	Gly	Phe	
				275					280					285		
Gln	Asp	Ala	Arg	Asp	Leu	Leu	Cys	Asn	Leu	Asn	Gly	Thr	Leu	Ala	Pro	
				290					295					300		
Ala	Thr	Trp	Gln	Gly	Ala	Leu	Gly	Cys	His	Tyr	Arg	Leu	Gly	Pro	Gly	
				305					310					315		
Phe	Arg	Pro	Asp	Gly	Asp	Phe	Pro	Ala	Asp	Ser	Gln	Val	Asn	Val	Ser	
				325					330					335		
Val	Tyr	Asn	Arg	Leu	Glu	Leu	Arg	Asn	Ser	Ser	Asn	Val	Leu	Gly	Ile	
				340					345					350		
Ile	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Leu	Tyr	Gly	Asn	His	
				355					360					365		
Arg	Asp	Ser	Trp	Val	His	Gly	Ala	Val	Asp	Pro	Ser	Ser	Gly	Thr	Ala	
				370					375					380		

Val	Leu	Leu	Glu	Leu	Ser	Arg	Val	Leu	Gly	Thr	Leu	Leu	Lys	Lys	Gly	385	390	395	400
Thr	Trp	Arg	Pro	Arg	Arg	Ser	Ile	Val	Phe	Ala	Ser	Trp	Gly	Ala	Glu	405	410	415	
Glu	Phe	Gly	Leu	Ile	Gly	Ser	Thr	Glu	Phe	Thr	Glu	Glu	Phe	Phe	Asn	420	425	430	
Lys	Leu	Gln	Glu	Arg	Thr	Val	Ala	Tyr	Ile	Asn	Val	Asp	Ile	Ser	Val	435	440	445	
Phe	Ala	Asn	Ala	Thr	Leu	Arg	Val	Gln	Gly	Thr	Pro	Pro	Val	Gln	Ser	450	455	460	
Val	Val	Phe	Ser	Ala	Thr	Lys	Glu	Ile	Arg	Ser	Pro	Gly	Pro	Gly	Asp	465	470	475	480
Leu	Ser	Ile	Tyr	Asp	Asn	Trp	Ile	Arg	Tyr	Phe	Asn	Arg	Ser	Ser	Pro	485	490	495	
Val	Tyr	Gly	Leu	Val	Pro	Ser	Leu	Gly	Ser	Leu	Gly	Ala	Gly	Ser	Asp	500	505	510	
Tyr	Ala	Pro	Phe	Val	His	Phe	Leu	Gly	Ile	Ser	Ser	Met	Asp	Ile	Ala	515	520	525	
Tyr	Thr	Tyr	Asp	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Ile	Tyr	Pro	Thr	Tyr	530	535	540	
His	Thr	Ala	Phe	Asp	Thr	Phe	Asp	Tyr	Val	Asp	Lys	Phe	Leu	Asp	Pro	545	550	555	560
Gly	Phe	Ser	Ser	His	Gln	Ala	Val	Ala	Arg	Thr	Ala	Gly	Ser	Val	Ile	565	570	575	
Leu	Arg	Leu	Ser	Asp	Ser	Phe	Phe	Leu	Pro	Leu	Lys	Val	Ser	Asp	Tyr	580	585	590	
Ser	Glu	Thr	Leu	Arg	Ser	Phe	Leu	Gln	Ala	Ala	Gln	Gln	Asp	Leu	Gly	595	600	605	
Ala	Leu	Leu	Glu	Gln	His	Ser	Ile	Ser	Leu	Gly	Pro	Leu	Val	Thr	Ala	610	615	620	
Val	Glu	Lys	Phe	Glu	Ala	Glu	Ala	Ala	Ala	Leu	Gly	Gln	Arg	Ile	Ser	625	630	635	640
Thr	Leu	Gln	Lys	Gly	Ser	Pro	Asp	Pro	Leu	Gln	Val	Arg	Met	Leu	Asn	645	650	655	
Asp	Gln	Leu	Met	Leu	Leu	Glu	Arg	Thr	Phe	Leu	Asn	Pro	Arg	Ala	Phe	660	665	670	
Pro	Glu	Glu	Arg	Tyr	Tyr	Ser	His	Val	Leu	Trp	Ala	Pro	Ser	His	Gly	675	680	685	

Leu Arg Ser His Ile Pro Gly Leu Ser Asn Ala Cys Ser Arg Ala Arg
 690 695 700
 Asp Thr Ala Ser Gly Ser Glu Ala Trp Ala Glu Val Gln Arg Gln Leu
 705 710 715 720
 Ser Ile Val Val Thr Ala Leu Glu Gly Ala Ala Ala Thr Leu Arg Pro
 725 730 735
 Val Ala Asp Leu
 740

<210> 36
 <211> 745
 <212> PRT
 <213> Rattus rattus

<400> 36
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 1 5 10 15
 Leu Gly Leu Gly Ile Ile Leu Gly His Phe Ala Ile Pro Lys Ala Thr
 20 25 30
 Glu Pro Leu Ala Ser Ser Val Ser Asp Ser Gln Asp Leu Asp Leu Ala
 35 40 45
 Ile Leu Asp Ser Val Met Gly Gln Leu Asp Ala Ser Arg Ile Arg Glu
 50 55 60
 Asn Leu Arg Glu Leu Ser Lys Glu Pro His Val Ala Thr Ser Ala Arg
 65 70 75 80
 Asp Glu Ala Leu Val Gln Leu Leu Leu Gly Arg Trp Lys Asp Ser Ala
 85 90 95
 Ser Gly Leu Asp Thr Ala Lys Thr Tyr Glu Tyr Thr Val Leu Leu Ser
 100 105 110
 Phe Pro Ser Thr Glu Gln Pro Asn Ser Val Glu Val Val Gly Pro Asn
 115 120 125
 Gly Thr Val Phe His Ser Phe Gln Pro Phe Glu Lys Asn Leu Thr Gly
 130 135 140
 Glu Gln Ala Glu Pro Asn Val Leu Gln Pro Tyr Ala Ala Tyr Ala Pro
 145 150 155 160
 Pro Gly Thr Pro Lys Gly Pro Leu Val Tyr Ala Asn Arg Gly Ser Glu
 165 170 175
 Asp Asp Phe Lys Lys Leu Glu Ala Glu Gly Ile Asn Leu Lys Gly Thr
 180 185 190
 Ile Ala Leu Thr Arg Tyr Gly Ser Val Gly Arg Gly Ala Lys Ala Ile
 195 200 205

Asn Ala Ala Arg His Gly Val Val Gly Val Leu Val Tyr Thr Asp Pro
 210 215 220
 Gly Asp Ile Asn Asp Gly Lys Ser Leu Pro Asn Glu Thr Phe Pro Asn
 225 230 235 240
 Ser Trp Gly Leu Pro Pro Ser Gly Val Glu Arg Gly Ser Tyr Tyr Glu
 245 250 255
 Tyr Phe Gly Asp Pro Leu Thr Pro Tyr Leu Pro Ala His Pro Val Ser
 260 265 270
 Phe Arg Leu Asp Pro His Asn Ile Ser Gly Phe Pro Pro Ile Pro Thr
 275 280 285
 Gln Pro Ile Gly Phe Glu Asp Ala Lys Asn Leu Leu Cys Asn Leu Asn
 290 295 300
 Gly Thr Ser Ala Pro Asp Ser Trp Gln Gly Ala Leu Gly Cys Glu Tyr
 305 310 315 320
 Lys Leu Gly Pro Gly Phe Glu Pro Asn Gly Asn Phe Pro Ala Gly Ser
 325 330 335
 Glu Val Lys Val Ser Val Tyr Asn Arg Leu Glu Leu Arg Asn Ser Ser
 340 345 350
 Asn Val Leu Gly Ile Ile Gln Gly Ala Val Glu Pro Asp Arg Tyr Val
 355 360 365
 Ile Tyr Gly Asn His Arg Asp Ser Trp Val His Gly Ala Val Asp Pro
 370 375 380
 Ser Ser Gly Thr Ala Val Leu Leu Glu Ile Ser Arg Val Leu Gly Thr
 385 390 395 400
 Leu Leu Lys Lys Gly Thr Trp Arg Pro Arg Arg Ser Ile Ile Phe Ala
 405 410 415
 Ser Trp Gly Ala Glu Glu Phe Gly Leu Ile Gly Ser Thr Glu Phe Thr
 420 425 430
 Glu Glu Phe Leu Ser Lys Leu Gln Glu Arg Thr Val Thr Tyr Ile Asn
 435 440 445
 Val Asp Ile Ser Val Phe Ser Asn Ala Thr Leu Arg Ala Gln Gly Thr
 450 455 460
 Pro Pro Val Gln Ser Val Ile Phe Ser Ala Thr Lys Glu Ile Ser Ala
 465 470 475 480
 Pro Gly Ser Ser Gly Leu Ser Ile Tyr Asp Asn Trp Ile Arg Tyr Thr
 485 490 495
 Asn Arg Ser Ser Pro Val Tyr Gly Leu Val Pro Ser Met Gly Thr Leu
 500 505 510

Gly Ala Gly Ser Asp Tyr Ala Ser Phe Ile His Phe Leu Gly Ile Thr
 515 520 525
 Ser Met Asp Leu Ala Tyr Thr Tyr Asp Arg Ser Lys Thr Ser Ala Arg
 530 535 540
 Ile Tyr Pro Thr Tyr His Thr Ala Phe Asp Thr Phe Asp Tyr Val Glu
 545 550 555 560
 Lys Phe Leu Asp Pro Gly Phe Ser Ser His Gln Ala Val Ala Arg Thr
 565 570 575
 Ala Gly Ser Val Leu Leu Arg Leu Ser Asp Ser Leu Phe Leu Pro Leu
 580 585 590
 Asn Val Ser Asp Tyr Ser Glu Thr Leu Gln Ser Phe Leu Gln Ala Ala
 595 600 605
 Gln Glu Asn Leu Gly Ala Leu Leu Glu Ser His Asn Ile Ser Leu Gly
 610 615 620
 Pro Leu Val Thr Ala Val Glu Lys Phe Lys Ala Ala Ala Ala Ala Leu
 625 630 635 640
 Asn Gln His Ile Leu Thr Leu Gln Lys Ser Ser Pro Asp Pro Leu Gln
 645 650 655
 Val Arg Met Val Asn Asp Gln Leu Met Leu Leu Glu Arg Ala Phe Leu
 660 665 670
 Asn Pro Arg Ala Phe Pro Glu Glu Arg Tyr Tyr Ser His Val Leu Trp
 675 680 685
 Ala Pro Asn Thr Ala Ser Val Ala Thr Phe Pro Gly Leu Ala Asn Ala
 690 695 700
 Tyr Ala Arg Ala Gln Glu Ile Asn Ser Gly Ala Glu Ala Trp Ala Glu
 705 710 715 720
 Val Glu Arg Gln Leu Ser Ile Ala Val Met Ala Leu Glu Gly Ala Ala
 725 730 735
 Ala Thr Leu Gln Pro Val Thr Asp Leu
 740 745

<210> 37

<211> 41

<212> PRT

<213> Homo sapiens

<400> 37

Gly Leu Leu Val Tyr Ala Asn Arg Gly Ala Glu Glu Asp Phe Lys Glu
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Leu Gln Thr Gln Gly Ile Lys Leu Glu Gly Thr Ile Ala Leu Thr Arg
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Tyr Gly Gly Val Gly Arg Gly Ala Lys
 35 40

<210> 38
 <211> 35
 <212> PRT
 <213> Homo sapiens

<400> 38
 Cys Asn Leu Asn Gly Thr Leu Ala Pro Ala Thr Trp Gln Gly Ala Leu
 1 5 10 15
 Gly Cys His Tyr Arg Leu Gly Pro Gly Phe Arg Pro Asp Gly Asp Phe
 20 25 30

Pro Ala Asp
 35

<210> 39
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 39
 Arg Leu Gln Gln Pro Ser Gly Cys Gly Pro Asp Ser Gly Glu Cys Asp
 1 5 10 15

Ser Pro Ala Gln
 20

<210> 40
 <211> 41
 <212> PRT
 <213> Homo sapiens

<400> 40
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 1 5 10 15

Pro Leu Thr Met Trp Thr Ser Phe Trp Thr Arg Ala Ser Ala Ala Ile
 20 25 30

Arg Leu Trp Pro Gly Gln Arg Gly Val
 35 40

<210> 41
 <211> 229
 <212> DNA
 <213> Homo sapiens

<400> 41
 gtgagcgtct acaaccgcct ggagctgagg aactcttcca acgtcctggg catcatccgt 60
 ggggctgtgg agcctgggtga gccctcctct tgctgcctgc accccaggcc cctgctctgc 120
 tctggatgcc gctgtectca tccagccctg cccttgccac caccagccc agctccccct 180

gccacacctt ccctctcctc tggttctctg ccccttttcc tctggccag

229

<210> 42

<211> 51

<212> PRT

<213> Homo sapiens

<400> 42

Gly Glu Pro Ser Ser Cys Cys Leu His Pro Arg Pro Leu Leu Cys Ser
1 5 10 15

Gly Cys Arg Cys Pro His Pro Ala Leu Pro Leu Pro Pro Pro Ser Pro
20 25 30

Ala Pro Pro Ala His Leu Ser Leu Ser Ser Gly Ser Leu Pro Leu Phe
35 40 45

Leu Trp Pro
50

<210> 43

<211> 82

<212> DNA

<213> Homo sapiens

<400> 43

gtgaggaggg agacaagggg catcctgaga ccaggacagg agaggctgaa gactgagccc 60
tggccttgtc accttgccgc ag 82

<210> 44

<211> 17

<212> PRT

<213> Homo sapiens

<400> 44

Glu Glu Gly Asp Lys Gly His Pro Glu Thr Arg Thr Gly Glu Ala Glu
1 5 10 15

Asp

<210> 45

<211> 74

<212> DNA

<213> Homo sapiens

<400> 45

gtatgcacag ccttgaccct gaggtatggg gagccctgca ccccatgac tgagccactg 60
cttgctcctc acag 74

<210> 46
 <211> 17
 <212> PRT
 <213> Homo sapiens

<400> 46
 Gly Met His Ser Pro Asp Pro Glu Val Trp Gly Ala Leu His Pro His
 1 5 10 15

Asp

<210> 47
 <211> 3110
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (12)..(2231)

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 1 5 10

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 Leu Ala Ala Ala Leu Ala Ser Phe Leu Met Gly Phe Met Val Gly Trp
 15 20 25

ttt att aag cct ctc aaa gaa aca acc act tct gtg cgc tat cat caa 146
 Phe Ile Lys Pro Leu Lys Glu Thr Thr Thr Ser Val Arg Tyr His Gln
 30 35 40 45

agt ata cgg tgg aaa ctg gta tcc gaa atg aaa gct gaa aac atc aaa 194
 Ser Ile Arg Trp Lys Leu Val Ser Glu Met Lys Ala Glu Asn Ile Lys
 50 55 60

tca ttt ctt cgt tct ttt aca aag ctt cct cat ctg gca gga aca gaa 242
 Ser Phe Leu Arg Ser Phe Thr Lys Leu Pro His Leu Ala Gly Thr Glu
 65 70 75

caa aat ttc ttg ctt gcc aag aaa atc caa acc cag tgg aag aaa ttt 290
 Gln Asn Phe Leu Leu Ala Lys Lys Ile Gln Thr Gln Trp Lys Lys Phe
 80 85 90

gga cta gat tca gcc aag ttg gtt cat tat gat gtc ctc tta tct tac 338
 Gly Leu Asp Ser Ala Lys Leu Val His Tyr Asp Val Leu Leu Ser Tyr
 95 100 105

ccc aat gag aca aat gcc aac tat ata tcg att gtg gat gaa cat gaa 386
 Pro Asn Glu Thr Asn Ala Asn Tyr Ile Ser Ile Val Asp Glu His Glu
 110 115 120 125

act gag att ttc aaa aca tca tac ctt gaa cca cca cca gat ggc tat 434
 Thr Glu Ile Phe Lys Thr Ser Tyr Leu Glu Pro Pro Pro Asp Gly Tyr
 130 135 140

gag aat gtt aca aat att gtg cca cca tat aat gct ttc tca gcc caa	482
Glu Asn Val Thr Asn Ile Val Pro Pro Tyr Asn Ala Phe Ser Ala Gln	
145 150 155	
ggc atg cca gag gga gat ctt gta tat gtg aac tat gct cgc act gaa	530
Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu	
160 165 170	
gac ttt ttc aaa cta gaa aga gag atg ggc atc aac tgt act ggg aag	578
Asp Phe Phe Lys Leu Glu Arg Glu Met Gly Ile Asn Cys Thr Gly Lys	
175 180 185	
att gtt att gca aga tat gga aaa atc ttc aga gga aat aaa gtt aaa	626
Ile Val Ile Ala Arg Tyr Gly Lys Ile Phe Arg Gly Asn Lys Val Lys	
190 195 200 205	
aat gcc atg tta gca gga gcc ata gga atc atc ttg tac tca gat cca	674
Asn Ala Met Leu Ala Gly Ala Ile Gly Ile Ile Leu Tyr Ser Asp Pro	
210 215 220	
gct gac tac ttt gct cct gag gta cag cca tat ccc aaa gga tgg aat	722
Ala Asp Tyr Phe Ala Pro Glu Val Gln Pro Tyr Pro Lys Gly Trp Asn	
225 230 235	
ctt cct gga act gca gcc cag aga gga aat gtg tta aat ttg aat ggt	770
Leu Pro Gly Thr Ala Ala Gln Arg Gly Asn Val Leu Asn Leu Asn Gly	
240 245 250	
gct ggt gac cca ctc act cca ggc tat cca gca aaa gaa tac act ttc	818
Ala Gly Asp Pro Leu Thr Pro Gly Tyr Pro Ala Lys Glu Tyr Thr Phe	
255 260 265	
aga ctt gat gtt gaa gaa gga gtg gga atc ccc cga ata cct gta cat	866
Arg Leu Asp Val Glu Glu Gly Val Gly Ile Pro Arg Ile Pro Val His	
270 275 280 285	
ccc att gga tat aat gat gca gaa ata tta tta cgc tac ttg gga gga	914
Pro Ile Gly Tyr Asn Asp Ala Glu Ile Leu Leu Arg Tyr Leu Gly Gly	
290 295 300	
att gct cca cca gat aag agt tgg aag gga gcc ctt aat gtg agt tat	962
Ile Ala Pro Pro Asp Lys Ser Trp Lys Gly Ala Leu Asn Val Ser Tyr	
305 310 315	
agt atc gga cct ggc ttt aca ggg agt gat tct ttc agg aag gtt aga	1010
Ser Ile Gly Pro Gly Phe Thr Gly Ser Asp Ser Phe Arg Lys Val Arg	
320 325 330	
atg cat gtt tat aac atc aat aaa att aca agg att tac aat gta gtt	1058
Met His Val Tyr Asn Ile Asn Lys Ile Thr Arg Ile Tyr Asn Val Val	
335 340 345	
gga act atc aga gga tct gtg gaa cct gac agg tat gtt att ctg gga	1106
Gly Thr Ile Arg Gly Ser Val Glu Pro Asp Arg Tyr Val Ile Leu Gly	
350 355 360 365	

ggt cac cgg gac tcc tgg gta ttt gga gct att gac cca acc agt ggg	1154
Gly His Arg Asp Ser Trp Val Phe Gly Ala Ile Asp Pro Thr Ser Gly	
370 375 380	
ggt gct gtt ttg caa gaa att gcc cgg agt ttt gga aaa ctg atg agt	1202
Val Ala Val Leu Gln Glu Ile Ala Arg Ser Phe Gly Lys Leu Met Ser	
385 390 395	
aaa ggc tgg aga cct aga aga act atc att ttt gcc agc tgg gat gca	1250
Lys Gly Trp Arg Pro Arg Arg Thr Ile Ile Phe Ala Ser Trp Asp Ala	
400 405 410	
gaa gaa ttt gga ctt ctg ggt tcc aca gaa tgg gct gag gag aat gtc	1298
Glu Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu Asn Val	
415 420 425	
aaa ata ctc cag gag aga agc att gct tat atc aac tcg gat tca tct	1346
Lys Ile Leu Gln Glu Arg Ser Ile Ala Tyr Ile Asn Ser Asp Ser Ser	
430 435 440 445	
ata gaa ggc aat tat act ctc aga gtt gac tgt act ccc ctt ctt tac	1394
Ile Glu Gly Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Leu Tyr	
450 455 460	
caa tta gtg tat aaa ctg aca aaa gag atc ccc agc cct gat gat ggg	1442
Gln Leu Val Tyr Lys Leu Thr Lys Glu Ile Pro Ser Pro Asp Asp Gly	
465 470 475	
ttt gag agt aaa tca ctg tat gaa agc tgg ttg gaa aaa gac cct tca	1490
Phe Glu Ser Lys Ser Leu Tyr Glu Ser Trp Leu Glu Lys Asp Pro Ser	
480 485 490	
cct gaa aat aaa aat ttg cct aga atc aat aag ctg gga tct gga agt	1538
Pro Glu Asn Lys Asn Leu Pro Arg Ile Asn Lys Leu Gly Ser Gly Ser	
495 500 505	
gac ttt gaa gct tat ttt cag aga ctt gga att gct tca ggc aga gcc	1586
Asp Phe Glu Ala Tyr Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala	
510 515 520 525	
cgt tac act aag aat aag aaa aca gat aag tac agc agc tac cca gtg	1634
Arg Tyr Thr Lys Asn Lys Lys Thr Asp Lys Tyr Ser Ser Tyr Pro Val	
530 535 540	
tac cac aca att tat gag aca ttt gaa ttg gta gag aaa ttt tat gac	1682
Tyr His Thr Ile Tyr Glu Thr Phe Glu Leu Val Glu Lys Phe Tyr Asp	
545 550 555	
ccc aca ttt aaa aaa caa ctt tct gtg gct caa tta cga gga gca ctg	1730
Pro Thr Phe Lys Lys Gln Leu Ser Val Ala Gln Leu Arg Gly Ala Leu	
560 565 570	
gta tat gag ctt gtg gat tct aaa atc att cct ttt aat att caa gac	1778
Val Tyr Glu Leu Val Asp Ser Lys Ile Ile Pro Phe Asn Ile Gln Asp	
575 580 585	

tat gca gaa gct ttg aaa aac tat gca gca agt atc tat aat cta tct	1826
Tyr Ala Glu Ala Leu Lys Asn Tyr Ala Ala Ser Ile Tyr Asn Leu Ser	
590 595 600 605	
aag aaa cat gat caa caa tta aca gac cat gga gta tca ttt gac tcc	1874
Lys Lys His Asp Gln Gln Leu Thr Asp His Gly Val Ser Phe Asp Ser	
610 615 620	
tta ttt tct gct gtg aaa aac ttc tca gag gct gct tca gat ttt cat	1922
Leu Phe Ser Ala Val Lys Asn Phe Ser Glu Ala Ala Ser Asp Phe His	
625 630 635	
aaa cga ctt ata caa gtt gat ctt aac aat ccc att gca gtg aga atg	1970
Lys Arg Leu Ile Gln Val Asp Leu Asn Asn Pro Ile Ala Val Arg Met	
640 645 650	
atg aat gac caa ctg atg ctc ctg gaa aga gca ttc atc gat cct ctt	2018
Met Asn Asp Gln Leu Met Leu Leu Glu Arg Ala Phe Ile Asp Pro Leu	
655 660 665	
ggc tta cca gga aag ctg ttc tat agc cac atc ata ttt gct cca agt	2066
Gly Leu Pro Gly Lys Leu Phe Tyr Arg His Ile Ile Phe Ala Pro Ser	
670 675 680 685	
agc cac aac aaa tat gct gga gaa tca ttt cct gga atc tat gat gct	2114
Ser His Asn Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala	
690 695 700	
atc ttt gat att gaa aat aaa gcc aac tct cgt ttg gcc tgg aaa gaa	2162
Ile Phe Asp Ile Glu Asn Lys Ala Asn Ser Arg Leu Ala Trp Lys Glu	
705 710 715	
gta aag aaa cat att tct att gca gct ttt aca att caa gca gca gca	2210
Val Lys Lys His Ile Ser Ile Ala Ala Phe Thr Ile Gln Ala Ala Ala	
720 725 730	
gga act ctg aaa gaa gta tta tagaaggtct caagtggcta gccattaaag	2261
Gly Thr Leu Lys Glu Val Leu	
735 740	
gtgttgctaa aagtctgagg ataaaattca cctttctgat aacttatgaa gccagggtgt	2321
tctaaactct tttcatgtca tgttttgatt ataggctttg gtcttttcat ctgcaaagcc	2381
tttttttttt ttgctcttta aaagttaata attatattag caaagtgtta atctaatagaa	2441
gtaaaaaact cctgtgtggc agaaagtaaa agaaaattcc cttaaattata gcaaggaaca	2501
tgaattctca gacattgtga gtgtgggaat gtaaaatggt aaaatcactt ttgaaaacag	2561
tttggcagtt tctataaag ttaaacatac acttttactt taggactcca gaattccact	2621
tctagttatt tattcaagag aaggaaaaac aatgatcaca gcaatacttg tatgcatgtt	2681
cattgcaact taaaagcgta aaaaccccaa atgtccatcc acagacgaat gtataaactg	2741
tggtatccat tacacaatag actacttact actcagcaat aaaaatgaag taactttcaa	2801

taaatgcaat attattggca gacattgttg aaggaaaaaa gccagacaaa caactacata 2861
 aaatatgttt ctatttagat gaagtggcaa actaatctgt agtgtaaaaa attagattag 2921
 tgattgcctg ggccaagtgg cagggtgggg aggatggctg caaagaagta tgaggaaact 2981
 ttctccaata gatgagaatt ttccgtatct tgatctgagt ggcaaattgt aaacttaaaa 3041
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<210> 48
 <211> 740
 <212> PRT
 <213> Homo sapiens

<400> 48
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 20 25 30
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 35 40 45
 Trp Lys Leu Val Ser Glu Met Lys Ala Glu Asn Ile Lys Ser Phe Leu
 50 55 60
 Arg Ser Phe Thr Lys Leu Pro His Leu Ala Gly Thr Glu Gln Asn Phe
 65 70 75 80
 Leu Leu Ala Lys Lys Ile Gln Thr Gln Trp Lys Lys Phe Gly Leu Asp
 85 90 95
 Ser Ala Lys Leu Val His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Glu
 100 105 110
 Thr Asn Ala Asn Tyr Ile Ser Ile Val Asp Glu His Glu Thr Glu Ile
 115 120 125
 Phe Lys Thr Ser Tyr Leu Glu Pro Pro Pro Asp Gly Tyr Glu Asn Val
 130 135 140
 Thr Asn Ile Val Pro Pro Tyr Asn Ala Phe Ser Ala Gln Gly Met Pro
 145 150 155 160
 Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe
 165 170 175
 Lys Leu Glu Arg Glu Met Gly Ile Asn Cys Thr Gly Lys Ile Val Ile
 180 185 190
 Ala Arg Tyr Gly Lys Ile Phe Arg Gly Asn Lys Val Lys Asn Ala Met
 195 200 205

Leu Ala Gly Ala Ile Gly Ile Ile Leu Tyr Ser Asp Pro Ala Asp Tyr
 210 215 220
 Phe Ala Pro Glu Val Gln Pro Tyr Pro Lys Gly Trp Asn Leu Pro Gly
 225 230 235 240
 Thr Ala Ala Gln Arg Gly Asn Val Leu Asn Leu Asn Gly Ala Gly Asp
 245 250 255
 Pro Leu Thr Pro Gly Tyr Pro Ala Lys Glu Tyr Thr Phe Arg Leu Asp
 260 265 270
 Val Glu Glu Gly Val Gly Ile Pro Arg Ile Pro Val His Pro Ile Gly
 275 280 285
 Tyr Asn Asp Ala Glu Ile Leu Leu Arg Tyr Leu Gly Gly Ile Ala Pro
 290 295 300
 Pro Asp Lys Ser Trp Lys Gly Ala Leu Asn Val Ser Tyr Ser Ile Gly
 305 310 315 320
 Pro Gly Phe Thr Gly Ser Asp Ser Phe Arg Lys Val Arg Met His Val
 325 330 335
 Tyr Asn Ile Asn Lys Ile Thr Arg Ile Tyr Asn Val Val Gly Thr Ile
 340 345 350
 Arg Gly Ser Val Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg
 355 360 365
 Asp Ser Trp Val Phe Gly Ala Ile Asp Pro Thr Ser Gly Val Ala Val
 370 375 380
 Leu Gln Glu Ile Ala Arg Ser Phe Gly Lys Leu Met Ser Lys Gly Trp
 385 390 395 400
 Arg Pro Arg Arg Thr Ile Ile Phe Ala Ser Trp Asp Ala Glu Glu Phe
 405 410 415
 Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu Asn Val Lys Ile Leu
 420 425 430
 Gln Glu Arg Ser Ile Ala Tyr Ile Asn Ser Asp Ser Ser Ile Glu Gly
 435 440 445
 Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Leu Tyr Gln Leu Val
 450 455 460
 Tyr Lys Leu Thr Lys Glu Ile Pro Ser Pro Asp Asp Gly Phe Glu Ser
 465 470 475 480
 Lys Ser Leu Tyr Glu Ser Trp Leu Glu Lys Asp Pro Ser Pro Glu Asn
 485 490 495
 Lys Asn Leu Pro Arg Ile Asn Lys Leu Gly Ser Gly Ser Asp Phe Glu
 500 505 510

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<210> 49
<211> 1884
<212> DNA
<213> Homo sapiens
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<221> CDS  
<222> (149)..(1564)
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taaacaagaa	aaccaactgg	aaaaaaaa	atg aaa ttc ctt atc ttc gca ttt			172
			Met Lys Phe Leu Ile Phe Ala Phe			
			1	5		
ttc ggt ggt gtt cac ctt tta tcc ctg tgc tct ggg aaa gct ata tgc						220
Phe Gly Gly Val His Leu Leu Ser Leu Cys Ser Gly Lys Ala Ile Cys						
	10		15	20		
aag aat ggc atc tct aag agg act ttt gaa gaa ata aaa gaa gaa ata						268
Lys Asn Gly Ile Ser Lys Arg Thr Phe Glu Glu Ile Lys Glu Glu Ile						
	25		30	35		40
gcc agc tgt gga gat gtt gct aaa gca atc atc aac cta gct gtt tat						316
Ala Ser Cys Gly Asp Val Ala Lys Ala Ile Ile Asn Leu Ala Val Tyr						
		45		50		55
ggt aaa gcc cag aac aga tcc tat gag cga ttg gca ctt ctg gtt gat						364
Gly Lys Ala Gln Asn Arg Ser Tyr Glu Arg Leu Ala Leu Leu Val Asp						
		60		65		70
act gtt gga ccc aga ctg agt ggc tcc aag aac cta gaa aaa gcc atc						412
Thr Val Gly Pro Arg Leu Ser Gly Ser Lys Asn Leu Glu Lys Ala Ile						
	75		80			85
caa att atg tac caa aac ctg cag caa gat ggg ctg gag aaa gtt cac						460
Gln Ile Met Tyr Gln Asn Leu Gln Gln Asp Gly Leu Glu Lys Val His						
	90		95			100
ctg gag cca gtg aga ata ccc cac tgg gag agg gga gaa gaa tca gct						508
Leu Glu Pro Val Arg Ile Pro His Trp Glu Arg Gly Glu Glu Ser Ala						
	105		110			120
gtg atg ctg gag cca aga att cat aag ata gcc atc ctg ggt ctt ggc						556
Val Met Leu Glu Pro Arg Ile His Lys Ile Ala Ile Leu Gly Leu Gly						
		125		130		135
agc agc att ggg act cct cca gaa ggc att aca gca gaa gtt ctg gtg						604
Ser Ser Ile Gly Thr Pro Pro Glu Gly Ile Thr Ala Glu Val Leu Val						
		140		145		150
gtg acc tct ttc gat gaa ctg cag aga agg gcc tca gaa gca aga ggg						652
Val Thr Ser Phe Asp Glu Leu Gln Arg Arg Ala Ser Glu Ala Arg Gly						
	155		160			165
aag att gtt gtt tat aac caa cct tac atc aac tac tca agg acg gtg						700
Lys Ile Val Val Tyr Asn Gln Pro Tyr Ile Asn Tyr Ser Arg Thr Val						
	170		175			180
caa tac cga acg cag ggg gcg gtg gaa gct gcc aag gtt ggg gct ttg						748
Gln Tyr Arg Thr Gln Gly Ala Val Glu Ala Ala Lys Val Gly Ala Leu						
	185		190			200
gca tct ctc att cga tcc gtg gcc tcc ttc tcc atc tac agt cct cac						796
Ala Ser Leu Ile Arg Ser Val Ala Ser Phe Ser Ile Tyr Ser Pro His						
		205		210		215

aca ggt att cag gaa tac cag gat ggc gtg ccc aag att cca aca gcc	844
Thr Gly Ile Gln Glu Tyr Gln Asp Gly Val Pro Lys Ile Pro Thr Ala	
220 225 230	
tgt att acg gtg gaa gat gca gaa atg atg tca aga atg gct tct cat	892
Cys Ile Thr Val Glu Asp Ala Glu Met Met Ser Arg Met Ala Ser His	
235 240 245	
ggg atc aaa att gtc att cag cta aag atg ggg gca aag acc tac cca	940
Gly Ile Lys Ile Val Ile Gln Leu Lys Met Gly Ala Lys Thr Tyr Pro	
250 255 260	
gat act gat tcc ttc aac act gta gca gag atc act ggg agc aaa tat	988
Asp Thr Asp Ser Phe Asn Thr Val Ala Glu Ile Thr Gly Ser Lys Tyr	
265 270 275 280	
cca gaa cag gtt gta ctg gtc agt gga cat ctg gac agc tgg gat gtt	1036
Pro Glu Gln Val Val Leu Val Ser Gly His Leu Asp Ser Trp Asp Val	
285 290 295	
ggg cag ggt gcc atg gat gat ggc ggt gga gcc ttt ata tca tgg gaa	1084
Gly Gln Gly Ala Met Asp Asp Gly Gly Ala Phe Ile Ser Trp Glu	
300 305 310	
gca ctc tca ctt att aaa gat ctt ggg ctg cgt cca aag agg act ctg	1132
Ala Leu Ser Leu Ile Lys Asp Leu Gly Leu Arg Pro Lys Arg Thr Leu	
315 320 325	
cgg ctg gtg ctc tgg act gca gaa gaa caa ggt gga gtt ggt gcc ttc	1180
Arg Leu Val Leu Trp Thr Ala Glu Glu Gln Gly Gly Val Gly Ala Phe	
330 335 340	
cag tat tat cag tta cac aag gta aat att tcc aac tac agt ctg gtg	1228
Gln Tyr Tyr Gln Leu His Lys Val Asn Ile Ser Asn Tyr Ser Leu Val	
345 350 355 360	
atg gag tct gac gca gga acc ttc tta ccc act ggg ctg caa ttc act	1276
Met Glu Ser Asp Ala Gly Thr Phe Leu Pro Thr Gly Leu Gln Phe Thr	
365 370 375	
ggc agt gaa aag gcc agg gcc atc atg gag gag gtt atg agc ctg ctg	1324
Gly Ser Glu Lys Ala Arg Ala Ile Met Glu Glu Val Met Ser Leu Leu	
380 385 390	
cag ccc ctc aat atc act cag gtc ctg agc cat gga gaa ggg aca gac	1372
Gln Pro Leu Asn Ile Thr Gln Val Leu Ser His Gly Glu Gly Thr Asp	
395 400 405	
atc aac ttt tgg atc caa gct gga gtg cct gga gcc agt cta ctt gat	1420
Ile Asn Phe Trp Ile Gln Ala Gly Val Pro Gly Ala Ser Leu Leu Asp	
410 415 420	
gac tta tac aag tat ttc ttc ttc cat cac tcc cac gga gac acc atg	1468
Asp Leu Tyr Lys Tyr Phe Phe Phe His His Ser His Gly Asp Thr Met	
425 430 435 440	

act gtc atg gat cca aag cag atg aat gtt gct gct gct gtt tgg gct 1516
 Thr Val Met Asp Pro Lys Gln Met Asn Val Ala Ala Ala Val Trp Ala
 445 450 455

gtt gtt tct tat gtt gtt gca gac atg gaa gaa atg ctg cct agg tcc 1564
 Val Val Ser Tyr Val Val Ala Asp Met Glu Glu Met Leu Pro Arg Ser
 460 465 470

tagaaacagt aagaaagaaa cgttttcatg cttctggcca ggaatcctgg gtctgcaact 1624
 ttggaaaact cctcttcaca taacaatttc atccaattca tcttcaaagc acaactctat 1684
 ttcattgcttt ctgttattat ctttcttgat actttccaaa ttctctgatt ctagaaaaag 1744
 gaatcattct cccctccctc ccaccacata gaatcaacat atggtaggga ttacagtggg 1804
 ggcatttctt tatatcacct cttaaaaaca ttgtttccac tttaaaagta aacacttaat 1864
 aaatTTTTTGG aagatctctg 1884

<210> 50

<211> 472

<212> PRT

<213> Homo sapiens

<400> 50

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
 1 5 10 15
 Leu Cys Ser Gly Lys Ala Ile Cys Lys Asn Gly Ile Ser Lys Arg Thr
 20 25 30
 Phe Glu Glu Ile Lys Glu Glu Ile Ala Ser Cys Gly Asp Val Ala Lys
 35 40 45
 Ala Ile Ile Asn Leu Ala Val Tyr Gly Lys Ala Gln Asn Arg Ser Tyr
 50 55 60
 Glu Arg Leu Ala Leu Leu Val Asp Thr Val Gly Pro Arg Leu Ser Gly
 65 70 75 80
 Ser Lys Asn Leu Glu Lys Ala Ile Gln Ile Met Tyr Gln Asn Leu Gln
 85 90 95
 Gln Asp Gly Leu Glu Lys Val His Leu Glu Pro Val Arg Ile Pro His
 100 105 110
 Trp Glu Arg Gly Glu Glu Ser Ala Val Met Leu Glu Pro Arg Ile His
 115 120 125
 Lys Ile Ala Ile Leu Gly Leu Gly Ser Ser Ile Gly Thr Pro Pro Glu
 130 135 140
 Gly Ile Thr Ala Glu Val Leu Val Val Thr Ser Phe Asp Glu Leu Gln
 145 150 155 160

Arg	Arg	Ala	Ser	Glu	Ala	Arg	Gly	Lys	Ile	Val	Val	Tyr	Asn	Gln	Pro	165	170	175
Tyr	Ile	Asn	Tyr	Ser	Arg	Thr	Val	Gln	Tyr	Arg	Thr	Gln	Gly	Ala	Val	180	185	190
Glu	Ala	Ala	Lys	Val	Gly	Ala	Leu	Ala	Ser	Leu	Ile	Arg	Ser	Val	Ala	195	200	205
Ser	Phe	Ser	Ile	Tyr	Ser	Pro	His	Thr	Gly	Ile	Gln	Glu	Tyr	Gln	Asp	210	215	220
Gly	Val	Pro	Lys	Ile	Pro	Thr	Ala	Cys	Ile	Thr	Val	Glu	Asp	Ala	Glu	225	230	235
Met	Met	Ser	Arg	Met	Ala	Ser	His	Gly	Ile	Lys	Ile	Val	Ile	Gln	Leu	245	250	255
Lys	Met	Gly	Ala	Lys	Thr	Tyr	Pro	Asp	Thr	Asp	Ser	Phe	Asn	Thr	Val	260	265	270
Ala	Glu	Ile	Thr	Gly	Ser	Lys	Tyr	Pro	Glu	Gln	Val	Val	Leu	Val	Ser	275	280	285
Gly	His	Leu	Asp	Ser	Trp	Asp	Val	Gly	Gln	Gly	Ala	Met	Asp	Asp	Gly	290	295	300
Gly	Gly	Ala	Phe	Ile	Ser	Trp	Glu	Ala	Leu	Ser	Leu	Ile	Lys	Asp	Leu	305	310	315
Gly	Leu	Arg	Pro	Lys	Arg	Thr	Leu	Arg	Leu	Val	Leu	Trp	Thr	Ala	Glu	325	330	335
Glu	Gln	Gly	Gly	Val	Gly	Ala	Phe	Gln	Tyr	Tyr	Gln	Leu	His	Lys	Val	340	345	350
Asn	Ile	Ser	Asn	Tyr	Ser	Leu	Val	Met	Glu	Ser	Asp	Ala	Gly	Thr	Phe	355	360	365
Leu	Pro	Thr	Gly	Leu	Gln	Phe	Thr	Gly	Ser	Glu	Lys	Ala	Arg	Ala	Ile	370	375	380
Met	Glu	Glu	Val	Met	Ser	Leu	Leu	Gln	Pro	Leu	Asn	Ile	Thr	Gln	Val	385	390	395
Leu	Ser	His	Gly	Glu	Gly	Thr	Asp	Ile	Asn	Phe	Trp	Ile	Gln	Ala	Gly	405	410	415
Val	Pro	Gly	Ala	Ser	Leu	Leu	Asp	Asp	Leu	Tyr	Lys	Tyr	Phe	Phe	Phe	420	425	430
His	His	Ser	His	Gly	Asp	Thr	Met	Thr	Val	Met	Asp	Pro	Lys	Gln	Met	435	440	445
Asn	Val	Ala	Ala	Ala	Val	Trp	Ala	Val	Val	Ser	Tyr	Val	Val	Ala	Asp	450	455	460

Met Glu Glu Met Leu Pro Arg Ser
465 470

<210> 51
<211> 750
<212> PRT
<213> Homo sapiens

<400> 51
Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
1 5 10 15
Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
20 25 30
Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
35 40 45
Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
50 55 60
Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His Asn Phe Thr Gln Ile
65 70 75 80
Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
85 90 95
Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
100 105 110
Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
115 120 125
Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
130 135 140
Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
145 150 155 160
Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
165 170 175
Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
180 185 190
Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
195 200 205
Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
210 215 220
Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
225 230 235 240
Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
245 250 255

Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
 260 265 270
 Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
 275 280 285
 Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
 290 295 300
 Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
 305 310 315 320
 Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
 325 330 335
 Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
 340 345 350
 Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
 355 360 365
 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
 370 375 380
 Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
 385 390 395 400
 Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
 405 410 415
 Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
 420 425 430
 Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
 435 440 445
 Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
 450 455 460
 Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
 465 470 475 480
 Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser
 485 490 495
 Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile
 500 505 510
 Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
 515 520 525
 Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
 530 535 540
 Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
 545 550 555 560

Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
565 570 575

Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
580 585 590

Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
595 600 605

Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
610 615 620

Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
625 630 635 640

Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
645 650 655

Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
660 665 670

Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
675 680 685

His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
690 695 700

Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
705 710 715 720

Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
725 730 735

Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
740 745 750

<210> 52

<211> 265

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 52

Thr Lys His Thr Val Ala Thr Val Gly Val Pro Tyr Lys Val Gly Lys
1 5 10 15

Lys Leu Ile Ala Asn Ile Ala Leu Asn Ile Asp Tyr Ser Leu Tyr Phe
20 25 30

Ala Met Asp Ser Tyr Val Glu Phe Ile Lys Thr Gln Asn Ile Ile Ala
35 40 45

Asp Thr Lys His Gly Asp Pro Asp Asn Ile Val Ala Leu Gly Ala His
50 55 60

Ser Asp Ser Val Glu Glu Gly Pro Gly Ile Asn Asp Asp Gly Ser Gly
65 70 75 80

Thr	Ile	Ser	Leu	Leu	Asn	Val	Ala	Lys	Gln	Leu	Thr	His	Phe	Lys	Ile	
				85					90					95		
Asn	Asn	Lys	Val	Arg	Phe	Ala	Trp	Trp	Ala	Ala	Glu	Glu	Glu	Gly	Leu	
				100					105					110		
Leu	Gly	Ser	Asn	Phe	Tyr	Ala	Tyr	Asn	Leu	Thr	Lys	Glu	Glu	Asn	Ser	
				115					120					125		
Lys	Ile	Arg	Val	Phe	Met	Asp	Tyr	Asp	Met	Met	Ala	Ser	Pro	Asn	Tyr	
				130					135					140		
Glu	Tyr	Glu	Ile	Tyr	Asp	Ala	Asn	Asn	Lys	Glu	Asn	Pro	Lys	Gly	Ser	
				145					150					155		
Glu	Glu	Leu	Lys	Asn	Leu	Tyr	Val	Asp	Tyr	Tyr	Lys	Ala	His	His	Leu	
				165					170					175		
Asn	Tyr	Thr	Leu	Val	Pro	Phe	Asp	Gly	Arg	Ser	Asp	Tyr	Val	Gly	Phe	
				180					185					190		
Ile	Asn	Asn	Gly	Ile	Pro	Ala	Gly	Gly	Ile	Ala	Thr	Gly	Ala	Glu	Lys	
				195					200					205		
Asn	Asn	Val	Asn	Asn	Gly	Lys	Val	Leu	Asp	Arg	Cys	Tyr	His	Gln	Leu	
				210					215					220		
Cys	Asp	Asp	Val	Ser	Asn	Leu	Ser	Trp	Asp	Ala	Phe	Ile	Thr	Asn	Thr	
				225					230					235		
Lys	Leu	Ile	Ala	His	Ser	Val	Ala	Thr	Tyr	Ala	Asp	Ser	Phe	Glu	Gly	
				245					250					255		
Phe	Pro	Lys	Arg	Glu	Thr	Gln	Lys	His								
				260					265							

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<210> .53  
<211> 268  
<212> PRT  
<213> Vibrio cholerae
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<400> 53																
Gln	Ile	Thr	Asn	Thr	Ile	Arg	Ala	Leu	Ser	Ser	Phe	Asn	Asn	Arg	Phe	
1				5					10					15		
Tyr	Thr	Thr	Ala	Ser	Gly	Ala	Gln	Ala	Ser	Asp	Trp	Leu	Ala	Asn	Glu	
			20					25					30			
Trp	Arg	Ser	Leu	Ile	Ser	Ser	Leu	Pro	Gly	Ser	Arg	Ile	Glu	Gln	Ile	
		35					40					45				
Lys	His	Ser	Gly	Tyr	Asn	Gln	Lys	Ser	Val	Val	Leu	Thr	Ile	Gln	Gly	
	50					55					60					
Ser	Glu	Lys	Pro	Asp	Glu	Trp	Val	Ile	Val	Gly	Gly	His	Leu	Asp	Ser	
65					70					75					80	

Thr	Leu	Gly	Ser	His	Thr	Asn	Glu	Gln	Ser	Ile	Ala	Pro	Gly	Ala	Asp	
				85					90							
Asp	Asp	Ala	Ser	Gly	Ile	Ala	Ser	Leu	Ser	Glu	Ile	Ile	Arg	Val	Leu	
				100					105							
Arg	Asp	Asn	Asn	Phe	Arg	Pro	Lys	Arg	Ser	Ala	Ala	Leu	Met	Ala	Tyr	
				115					120							
Ala	Ala	Glu	Glu	Val	Gly	Leu	Arg	Gly	Ser	Gln	Asp	Pro	Ala	Asn	Gln	
				130					135							
Tyr	Lys	Ala	Gln	Gly	Lys	Lys	Val	Val	Ser	Val	Leu	Gln	Leu	Asp	Met	
145					150					155						
Thr	Asn	Tyr	Arg	Gly	Ser	Ala	Glu	Asp	Ile	Val	Phe	Ile	Thr	Asp	Tyr	
				165					170							
Thr	Asp	Ser	Asn	Leu	Thr	Gln	Phe	Leu	Thr	Thr	Leu	Ile	Asp	Glu	Tyr	
				180					185							
Leu	Pro	Glu	Leu	Thr	Tyr	Gly	Tyr	Asp	Arg	Cys	Gly	Tyr	Ala	Cys	Ser	
				195					200							
Asp	His	Ala	Ser	Trp	His	Lys	Ala	Gly	Phe	Ser	Ala	Ala	Met	Pro	Phe	
				210					215							
Glu	Ser	Lys	Phe	Lys	Asp	Tyr	Asn	Pro	Lys	Ile	His	Thr	Ser	Gln	Asp	
225					230					235						
Thr	Leu	Ala	Asn	Ser	Asp	Pro	Thr	Gly	Asn	His	Ala	Val	Thr	Phe	Thr	
				245					250							
Lys	Leu	Gly	Leu	Ala	Tyr	Val	Ile	Glu	Met	Ala	Asn					
				260					265							

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<210> 54
<211> 268
<212> PRT
<213> Aeromonas proteolytica
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<400> 54
Gln Ile Thr Gly Thr Ile Ser Ser Leu Glu Ser Phe Thr Asn Arg Phe
  1                               10                      15

Tyr Thr Thr Thr Ser Gly Ala Gln Ala Ser Asp Trp Ile Ala Ser Glu
          20                      25                      30

Trp Gln Ala Leu Ser Ala Ser Leu Pro Asn Ala Ser Val Lys Gln Val
          35                      40                      45

Ser His Ser Gly Tyr Asn Gln Lys Ser Val Val Met Thr Ile Thr Gly
          50                      55                      60

Ser Glu Ala Pro Asp Glu Trp Ile Val Ile Gly Gly His Leu Asp Ser
          65                      70                      75                      80

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Thr Ile Gly Ser His Thr Asn Glu Gln Ser Val Ala Pro Gly Ala Asp
 85 90 95
 Asp Asp Ala Ser Gly Ile Ala Ala Val Thr Glu Val Ile Arg Val Leu
 100 105 110
 Ser Glu Asn Asn Phe Gln Pro Lys Arg Ser Ile Ala Phe Met Ala Tyr
 115 120 125
 Ala Ala Glu Glu Val Gly Leu Arg Gly Ser Gln Asp Leu Ala Asn Gln
 130 135 140
 Tyr Lys Ser Glu Gly Lys Asn Val Val Ser Ala Leu Gln Leu Asp Met
 145 150 155 160
 Thr Asn Tyr Lys Gly Ser Ala Gln Asp Val Val Phe Ile Thr Asp Tyr
 165 170 175
 Thr Asp Ser Asn Phe Thr Gln Tyr Leu Thr Gln Leu Met Asp Glu Tyr
 180 185 190
 Leu Pro Ser Leu Thr Tyr Gly Phe Asp Thr Cys Gly Tyr Ala Cys Ser
 195 200 205
 Asp His Ala Ser Trp His Asn Ala Gly Tyr Pro Ala Ala Met Pro Phe
 210 215 220
 Glu Ser Lys Phe Asn Asp Tyr Asn Pro Arg Ile His Thr Thr Gln Asp
 225 230 235 240
 Thr Leu Ala Asn Ser Asp Pro Thr Gly Ser His Ala Lys Lys Phe Thr
 245 250 255
 Gln Leu Gly Leu Ala Tyr Ala Ile Glu Met Gly Ser
 260 265

<210> 55

<211> 263

<212> PRT

<213> Streptomyces griseus

<400> 55

Asn Asn Gly Gly Asn Arg Ala His Gly Arg Pro Gly Tyr Lys Ala Ser
 1 5 10 15
 Val Asp Tyr Val Lys Ala Lys Leu Asp Ala Ala Gly Tyr Thr Thr Thr
 20 25 30
 Leu Gln Gln Phe Thr Ser Gly Gly Ala Thr Gly Tyr Asn Leu Ile Ala
 35 40 45
 Asn Trp Pro Gly Gly Asp Pro Asn Lys Val Leu Met Ala Gly Ala His
 50 55 60
 Leu Asp Ser Val Ser Ser Gly Ala Gly Ile Asn Asp Asn Gly Ser Gly
 65 70 75 80

Ser Ala Ala Val Leu Glu Thr Ala Leu Ala Val Ser Arg Ala Gly Tyr
 85 90 95
 Gln Pro Asp Lys His Leu Arg Phe Ala Trp Trp Gly Ala Glu Glu Leu
 100 105 110
 Gly Leu Ile Gly Ser Lys Phe Tyr Val Asn Asn Leu Pro Ser Ala Asp
 115 120 125
 Arg Ser Lys Leu Ala Gly Tyr Leu Asn Phe Asp Met Ile Gly Ser Pro
 130 135 140
 Asn Pro Gly Tyr Phe Val Tyr Asp Asp Asp Pro Val Ile Glu Lys Thr
 145 150 155 160
 Phe Lys Asn Tyr Phe Ala Gly Leu Asn Val Pro Thr Glu Ile Glu Thr
 165 170 175
 Glu Gly Asp Gly Arg Ser Asp His Ala Pro Phe Lys Asn Val Gly Val
 180 185 190
 Pro Val Gly Gly Leu Phe Thr Gly Ala Gly Tyr Thr Lys Ser Ala Ala
 195 200 205
 Gln Ala Gln Lys Trp Gly Gly Thr Ala Gly Gln Ala Phe Asp Arg Cys
 210 215 220
 Tyr His Ser Ser Cys Asp Ser Leu Ser Asn Ile Asn Asp Thr Ala Leu
 225 230 235 240
 Asp Arg Asn Ser Asp Ala Ala Ala His Ala Ile Trp Thr Leu Ser Ser
 245 250 255
 Gly Thr Gly Glu Pro Pro Thr
 260

<210> 56
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 56
 Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp
 1 5 10 15
 Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly
 20 25 30
 Phe Thr Gly Asn Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser
 35 40 45
 Thr Asn Glu Val Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly
 50 55 60
 Ala Val Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser
 65 70 75 80

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<210> 57
<211> 282
<212> PRT
<213> Homo sapiens
```

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<400> 57
Asp Ala Glu Ile Leu Leu Arg Tyr Leu Gly Gly Ile Ala Pro Pro Asp
  1             5             10             15

Lys Ser Trp Lys Gly Ala Leu Asn Val Ser Tyr Ser Ile Gly Pro Gly
      20             25             30

Phe Thr Gly Ser Asp Ser Phe Arg Lys Val Arg Met His Val Tyr Asn
      35             40             45

Ile Asn Lys Ile Thr Arg Ile Tyr Asn Val Val Gly Thr Ile Arg Gly
  50             55             60

```

Ser Val Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser
 65 70 75 80
 Trp Val Phe Gly Ala Ile Asp Pro Thr Ser Gly Val Ala Val Leu Gln
 85 90 95
 Glu Ile Ala Arg Ser Phe Gly Lys Leu Met Ser Lys Gly Trp Arg Pro
 100 105 110
 Arg Arg Thr Ile Ile Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu
 115 120 125
 Leu Gly Ser Thr Glu Trp Ala Glu Glu Asn Val Lys Ile Leu Gln Glu
 130 135 140
 Arg Ser Ile Ala Tyr Ile Asn Ser Asp Ser Ser Ile Glu Gly Asn Tyr
 145 150 155 160
 Thr Leu Arg Val Asp Cys Thr Pro Leu Leu Tyr Gln Leu Val Tyr Lys
 165 170 175
 Leu Thr Lys Glu Ile Pro Ser Pro Asp Asp Gly Phe Glu Ser Lys Ser
 180 185 190
 Leu Tyr Glu Ser Trp Leu Glu Lys Asp Pro Ser Pro Glu Asn Lys Asn
 195 200 205
 Leu Pro Arg Ile Asn Lys Leu Gly Ser Gly Ser Asp Phe Glu Ala Tyr
 210 215 220
 Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn
 225 230 235 240
 Lys Lys Thr Asp Lys Tyr Ser Ser Tyr Pro Val Tyr His Thr Ile Tyr
 245 250 255
 Glu Thr Phe Glu Leu Val Glu Lys Phe Tyr Asp Pro Thr Phe Lys Lys
 260 265 270
 Gln Leu Ser Val Ala Gln Leu Arg Gly Ala
 275 280

<210> 58

<211> 283

<212> PRT

<213> Homo sapiens

<400> 58

Arg Asp Leu Leu Cys Asn Leu Asn Gly Thr Leu Ala Pro Ala Thr Trp
 1 5 10 15
 Gln Gly Ala Leu Gly Cys His Tyr Arg Leu Gly Pro Gly Phe Arg Pro
 20 25 30
 Asp Gly Asp Phe Pro Ala Asp Ser Gln Val Asn Val Ser Val Tyr Asn
 35 40 45

Arg Leu Glu Leu Arg Asn Ser Ser Asn Val Leu Gly Ile Ile Arg Gly
 50 55 60
 Ala Val Glu Pro Asp Arg Tyr Val Leu Tyr Gly Asn His Arg Asp Ser
 65 70 75 80
 Trp Val His Gly Ala Val Asp Pro Ser Ser Gly Thr Ala Val Leu Leu
 85 90 95
 Glu Leu Ser Arg Val Leu Gly Thr Leu Leu Lys Lys Gly Thr Trp Arg
 100 105 110
 Pro Arg Arg Ser Ile Val Phe Ala Ser Trp Gly Ala Glu Glu Phe Gly
 115 120 125
 Leu Ile Gly Ser Thr Glu Phe Thr Glu Glu Phe Phe Asn Lys Leu Gln
 130 135 140
 Glu Arg Thr Val Ala Tyr Ile Asn Val Asp Ile Ser Val Phe Ala Asn
 145 150 155 160
 Ala Thr Leu Arg Val Gln Gly Thr Pro Pro Val Gln Ser Val Val Phe
 165 170 175
 Ser Ala Thr Lys Glu Ile Arg Ser Pro Gly Pro Gly Asp Leu Ser Ile
 180 185 190
 Tyr Asp Asn Trp Ile Arg Tyr Phe Asn Arg Ser Ser Pro Val Tyr Gly
 195 200 205
 Leu Val Pro Ser Leu Gly Ser Leu Gly Ala Gly Ser Asp Tyr Ala Pro
 210 215 220
 Phe Val His Phe Leu Gly Ile Ser Ser Met Asp Ile Ala Tyr Thr Tyr
 225 230 235 240
 Asp Arg Ser Lys Thr Ser Ala Arg Ile Tyr Pro Thr Tyr His Thr Ala
 245 250 255
 Phe Asp Thr Phe Asp Tyr Val Asp Lys Phe Leu Asp Pro Gly Phe Ser
 260 265 270
 Ser His Gln Ala Val Ala Arg Thr Ala Gly Ser
 275 280

<210> 59

<211> 259

<212> PRT

<213> Homo sapiens

<400> 59

Ser Pro His Thr Gly Ile Gln Glu Tyr Gln Asp Gly Val Pro Lys Ile
 1 5 10 15

Pro Thr Ala Cys Ile Thr Val Glu Asp Ala Glu Met Met Ser Arg Met
 20 25 30

Ala Ser His Gly Ile Lys Ile Val Ile Gln Leu Lys Met Gly Ala Lys
 35 40 45

Thr Tyr Pro Asp Thr Asp Ser Phe Asn Thr Val Ala Glu Ile Thr Gly
 50 55 60

Ser Lys Tyr Pro Glu Gln Val Val Leu Val Ser Gly His Leu Asp Ser
 65 70 75 80

Trp Asp Val Gly Gln Gly Ala Met Asp Asp Gly Gly Gly Ala Phe Ile
 85 90 95

Ser Trp Glu Ala Leu Ser Leu Ile Lys Asp Leu Gly Leu Arg Pro Lys
 100 105 110

Arg Thr Leu Arg Leu Val Leu Trp Thr Ala Glu Glu Gln Gly Gly Val
 115 120 125

Gly Ala Phe Gln Tyr Tyr Gln Leu His Lys Val Asn Ile Ser Asn Tyr
 130 135 140

Ser Leu Val Met Glu Ser Asp Ala Gly Thr Phe Leu Pro Thr Gly Leu
 145 150 155 160

Gln Phe Thr Gly Ser Glu Lys Ala Arg Ala Ile Met Glu Glu Val Met
 165 170 175

Ser Leu Leu Gln Pro Leu Asn Ile Thr Gln Val Leu Ser His Gly Glu
 180 185 190

Gly Thr Asp Ile Asn Phe Trp Ile Gln Ala Gly Val Pro Gly Ala Ser
 195 200 205

Leu Leu Asp Asp Leu Tyr Lys Tyr Phe Phe Phe His His Ser His Gly
 210 215 220

Asp Thr Met Thr Val Met Asp Pro Lys Gln Met Asn Val Ala Ala Ala
 225 230 235 240

Val Trp Ala Val Val Ser Tyr Val Val Ala Asp Met Glu Glu Met Leu
 245 250 255

Pro Arg Ser

<210> 60

<211> 2197

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (315)

<223> a, c, g, t, unknown or other

<400> 60

gccaaagatgc cgcaggatgc agtggacgaa ggtgttgggg ctggggctgg gggctgctgc 60

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ggccccccag gacctggacc tggagatcct ggagaccgtc atggggcagc tggatgccc 180
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<211> 699

<212> PRT

<213> Homo sapiens

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<223> variable amino acid

<400> 61

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Asn Ser Leu Ala Pro Gln Asp Leu Asp Leu Glu Ile Leu Glu Thr Val
35 40 45

Met Gly Gln Leu Asp Ala His Arg Ile Arg Glu Asn Leu Arg Glu Leu
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 Ser Arg Glu Pro His Leu Ala Ser Ser Pro Arg Asp Glu Asp Leu Val
 65 70 75 80
 Gln Leu Leu Leu Gln Arg Trp Lys Asp Pro Glu Ser Gly Leu Asp Ser
 85 90 95
 Ala Glu Ala Xaa Thr Tyr Glu Val Leu Leu Ser Phe Pro Ser Gln Glu
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 115 120 125
 Ser Cys His Arg Thr Glu Glu Asn Val Thr Gly Glu Gln Gly Gly Pro
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 Asp Val Val Gln Pro Tyr Ala Ala Tyr Ala Pro Ser Gly Thr Pro Gln
 145 150 155 160
 Ala Val Asn Ala Ala Lys His Gly Val Ala Gly Val Leu Val Tyr Thr
 165 170 175
 Asp Pro Ala Asp Ile Asn Asp Gly Leu Ser Ser Pro Asp Glu Thr Phe
 180 185 190
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 195 200 205
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 His Tyr Arg Leu Gly Pro Gly Phe Arg Pro Asp Gly Asp Phe Pro Ala
 275 280 285
 Asp Ser Gln Val Asn Val Ser Val Tyr Asn Arg Leu Glu Leu Arg Asn
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 Ser Ser Asn Val Leu Gly Ile Ile Arg Gly Ala Val Glu Pro Asp Arg
 305 310 315 320
 Tyr Val Leu Tyr Gly Asn His Arg Asp Ser Trp Val His Gly Ala Val
 325 330 335
 Asp Pro Ser Ser Gly Thr Ala Val Leu Leu Glu Leu Ser Arg Val Leu
 340 345 350

Gly Thr Leu Leu Lys Lys Gly Thr Trp Arg Pro Arg Arg Ser Ile Val
 355 360 365
 Phe Ala Ser Trp Gly Ala Glu Glu Phe Gly Leu Ile Gly Ser Thr Glu
 370 375 380
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 385 390 395 400
 Ile Asn Val Asp Ile Ser Val Phe Ala Asn Ala Thr Leu Arg Val Gln
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 Gly Thr Pro Pro Val Gln Ser Val Val Phe Ser Ala Thr Lys Glu Ile
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 Pro Leu Lys Val Ser Asp Tyr Ser Glu Thr Leu Arg Ser Phe Leu Gln
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 Leu Gly Pro Leu Val Thr Ala Val Glu Lys Phe Glu Ala Glu Ala Ala
 580 585 590
 Ala Leu Gly Gln Arg Ile Ser Thr Leu Gln Lys Gly Ser Pro Asp Pro
 595 600 605
 Leu Gln Val Arg Met Leu Asn Asp Gln Leu Met Leu Leu Glu Arg Thr
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 Phe Leu Asn Pro Arg Ala Phe Pro Glu Glu Arg Tyr Tyr Ser His Val
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 645 650 655

Asn Ala Cys Ser Arg Ala Arg Asp Thr Ala Ser Gly Ser Glu Ala Trp
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Ala Ala Ala Thr Leu Arg Pro Val Ala Asp Leu
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<212> DNA

<213> Homo sapiens

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<223> a, c, g, t, unknown or other

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 <212> PRT
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 Asn Ser Leu Ala Pro Gln Asp Leu Asp Leu Glu Ile Leu Glu Thr Val
 35 40 45
 Met Gly Gln Leu Asp Ala His Arg Ile Arg Glu Asn Leu Arg Glu Leu
 50 55 60
 Ser Arg Glu Pro His Leu Ala Ser Ser Pro Arg Asp Glu Asp Leu Val
 65 70 75 80
 Gln Leu Leu Leu Gln Arg Trp Lys Asp Pro Glu Ser Gly Leu Asp Ser
 85 90 95
 Ala Glu Ala Xaa Thr Tyr Glu Val Leu Leu Ser Phe Pro Ser Gln Glu
 100 105 110
 Gln Pro Asn Val Val Asp Ile Val Gly Pro Thr Gly Gly Ile Ile His
 115 120 125
 Ser Cys His Arg Thr Glu Glu Asn Val Thr Gly Glu Gln Gly Gly Pro
 130 135 140
 Asp Val Val Gln Pro Tyr Ala Ala Tyr Ala Pro Ser Gly Thr Pro Gln
 145 150 155 160
 Gly Leu Leu Val Tyr Ala Asn Arg Gly Ala Glu Glu Asp Phe Lys Glu
 165 170 175
 Leu Gln Thr Gln Gly Ile Lys Leu Glu Gly Thr Ile Ala Leu Thr Arg
 180 185 190
 Tyr Gly Gly Val Gly Arg Gly Ala Lys Ala Val Asn Ala Ala Lys His
 195 200 205
 Gly Val Ala Gly Val Leu Val Tyr Thr Asp Pro Ala Asp Ile Asn Asp
 210 215 220
 Gly Leu Ser Ser Pro Asp Glu Thr Phe Pro Asn Ser Trp Tyr Leu Pro
 225 230 235 240

Pro	Ser	Gly	Val	Glu	Arg	Gly	Ser	Tyr	Tyr	Glu	Tyr	Phe	Gly	Asp	Pro	245	250	255
Leu	Thr	Pro	Tyr	Leu	Pro	Ala	Val	Pro	Ser	Ser	Phe	Arg	Val	Asp	Leu	260	265	270
Ala	Asn	Val	Ser	Gly	Phe	Pro	Pro	Ile	Pro	Thr	Gln	Pro	Ile	Gly	Phe	275	280	285
Gln	Asp	Ala	Arg	Asp	Leu	Leu	Ser	Gln	Val	Asn	Val	Ser	Val	Tyr	Asn	290	295	300
Arg	Leu	Glu	Leu	Arg	Asn	Ser	Ser	Asn	Val	Leu	Gly	Ile	Ile	Arg	Gly	305	310	315
Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Leu	Tyr	Gly	Asn	His	Arg	Asp	Ser	325	330	335
Trp	Val	His	Gly	Ala	Val	Asp	Pro	Ser	Ser	Gly	Thr	Ala	Val	Leu	Leu	340	345	350
Glu	Leu	Ser	Arg	Val	Leu	Gly	Thr	Leu	Leu	Lys	Lys	Gly	Thr	Trp	Arg	355	360	365
Pro	Arg	Arg	Ser	Ile	Val	Phe	Ala	Ser	Trp	Gly	Ala	Glu	Glu	Phe	Gly	370	375	380
Leu	Ile	Gly	Ser	Thr	Glu	Phe	Thr	Glu	Glu	Phe	Phe	Asn	Lys	Leu	Gln	385	390	395
Glu	Arg	Thr	Val	Ala	Tyr	Ile	Asn	Val	Asp	Ile	Ser	Val	Phe	Ala	Asn	405	410	415
Ala	Thr	Leu	Arg	Val	Gln	Gly	Thr	Pro	Pro	Val	Gln	Ser	Val	Val	Phe	420	425	430
Ser	Ala	Thr	Lys	Glu	Ile	Arg	Ser	Pro	Gly	Pro	Gly	Asp	Leu	Ser	Ile	435	440	445
Tyr	Asp	Asn	Trp	Ile	Arg	Tyr	Phe	Asn	Arg	Ser	Ser	Pro	Val	Tyr	Gly	450	455	460
Leu	Val	Pro	Ser	Leu	Gly	Ser	Leu	Gly	Ala	Gly	Ser	Asp	Tyr	Ala	Pro	465	470	475
Phe	Val	His	Phe	Leu	Gly	Ile	Ser	Ser	Met	Asp	Ile	Ala	Tyr	Thr	Tyr	485	490	495
Asp	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Ile	Tyr	Pro	Thr	Tyr	His	Thr	Ala	500	505	510
Phe	Asp	Thr	Phe	Asp	Tyr	Val	Asp	Lys	Phe	Leu	Asp	Pro	Gly	Phe	Ser	515	520	525
Ser	His	Gln	Ala	Val	Ala	Arg	Thr	Ala	Gly	Ser	Val	Ile	Leu	Arg	Leu	530	535	540

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 Glu Gln His Ser Ile Ser Leu Gly Pro Leu Val Thr Ala Val Glu Lys
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 Arg Tyr Tyr Ser His Val Leu Trp Ala Pro Ser His Gly Leu Arg Ser
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 Ser Gly Ser Glu Ala Trp Ala Glu Val Gln Arg Gln Leu Ser Ile Val
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 <212> DNA
 <213> Homo sapiens

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 <222> (315)
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<210> 65
 <211> 791
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 <213> Homo sapiens

<220>
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 <222> (100)
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 35 40 45
 Met Gly Gln Leu Asp Ala His Arg Ile Arg Glu Asn Leu Arg Glu Leu
 50 55 60
 Ser Arg Glu Pro His Leu Ala Ser Ser Pro Arg Asp Glu Asp Leu Val
 65 70 75 80

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Gln	Pro	Asn	Val	Val	Asp	Ile	Val	Gly	Pro	Thr	Gly	Gly	Ile	Ile	His
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305					310					315					320
Phe	Arg	Pro	Asp	Gly	Asp	Phe	Pro	Ala	Asp	Ser	Gln	Val	Asn	Val	Ser
				325					330					335	
Val	Tyr	Asn	Arg	Leu	Glu	Leu	Arg	Asn	Ser	Ser	Asn	Val	Leu	Gly	Ile
				340				345					350		
Ile	Arg	Gly	Ala	Val	Glu	Pro	Gly	Glu	Pro	Ser	Ser	Cys	Cys	Leu	His
				355			360					365			
Pro	Arg	Pro	Leu	Leu	Cys	Ser	Gly	Cys	Arg	Cys	Pro	His	Pro	Ala	Leu
				370		375					380				

Pro Leu Pro Pro Pro Ser Pro Ala Pro Pro Ala His Leu Ser Leu Ser
 385 390 395 400
 Ser Gly Ser Leu Pro Leu Phe Leu Trp Pro Asp Arg Tyr Val Leu Tyr
 405 410 415
 Gly Asn His Arg Asp Ser Trp Val His Gly Ala Val Asp Pro Ser Ser
 420 425 430
 Gly Thr Ala Val Leu Leu Glu Leu Ser Arg Val Leu Gly Thr Leu Leu
 435 440 445
 Lys Lys Gly Thr Trp Arg Pro Arg Arg Ser Ile Val Phe Ala Ser Trp
 450 455 460
 Gly Ala Glu Glu Phe Gly Leu Ile Gly Ser Thr Glu Phe Thr Glu Glu
 465 470 475 480
 Phe Phe Asn Lys Leu Gln Glu Arg Thr Val Ala Tyr Ile Asn Val Asp
 485 490 495
 Ile Ser Val Phe Ala Asn Ala Thr Leu Arg Val Gln Gly Thr Pro Pro
 500 505 510
 Val Gln Ser Val Val Phe Ser Ala Thr Lys Glu Ile Arg Ser Pro Gly
 515 520 525
 Pro Gly Asp Leu Ser Ile Tyr Asp Asn Trp Ile Arg Tyr Phe Asn Arg
 530 535 540
 Ser Ser Pro Val Tyr Gly Leu Val Pro Ser Leu Gly Ser Leu Gly Ala
 545 550 555 560
 Gly Ser Asp Tyr Ala Pro Phe Val His Phe Leu Gly Ile Ser Ser Met
 565 570 575
 Asp Ile Ala Tyr Thr Tyr Asp Arg Ser Lys Thr Ser Ala Arg Ile Tyr
 580 585 590
 Pro Thr Tyr His Thr Ala Phe Asp Thr Phe Asp Tyr Val Asp Lys Phe
 595 600 605
 Leu Asp Pro Gly Phe Ser Ser His Gln Ala Val Ala Arg Thr Ala Gly
 610 615 620
 Ser Val Ile Leu Arg Leu Ser Asp Ser Phe Phe Leu Pro Leu Lys Val
 625 630 635 640
 Ser Asp Tyr Ser Glu Thr Leu Arg Ser Phe Leu Gln Ala Ala Gln Gln
 645 650 655
 Asp Leu Gly Ala Leu Leu Glu Gln His Ser Ile Ser Leu Gly Pro Leu
 660 665 670
 Val Thr Ala Val Glu Lys Phe Glu Ala Glu Ala Ala Ala Leu Gly Gln
 675 680 685

Arg Ile Ser Thr Leu Gln Lys Gly Ser Pro Asp Pro Leu Gln Val Arg
 690 695 700
 Met Leu Asn Asp Gln Leu Met Leu Leu Glu Arg Thr Phe Leu Asn Pro
 705 710 715 720
 Arg Ala Phe Pro Glu Glu Arg Tyr Tyr Ser His Val Leu Trp Ala Pro
 725 730 735
 Ser His Gly Leu Arg Ser His Ile Pro Gly Leu Ser Asn Ala Cys Ser
 740 745 750
 Arg Ala Arg Asp Thr Ala Ser Gly Ser Glu Ala Trp Ala Glu Val Gln
 755 760 765
 Arg Gln Leu Ser Ile Val Val Thr Ala Leu Glu Gly Ala Ala Ala Thr
 770 775 780
 Leu Arg Pro Val Ala Asp Leu
 785 790

<210> 66
 <211> 2402
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> a, c, g, t, unknown or other

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 ggccccccag gacctggacc tggagatcct ggagaccgtc atggggcagc tggatgccca 180
 caggatccgg gagaacctca gagaactctc cagggagcca caactggcct ccagccctcg 240
 ggatgaggac ctggtgcagc tgctgctgca gcgctggaag gaccagagt caggcctgga 300
 ctcgccgag gctncacgt acgaagtgt gctgtccttc cctagccagg agcagcccaa 360
 cgtcgtggac atcgtgggcc ccactggggg catcatccac tcctgccacc ggactgagga 420
 gaacgtgacc ggggagcaag gggggccaga tgtggtacaa ccctatgctg cctatgctcc 480
 ttctggaacc ccacagggcc tcctcgtcta tgccaaccgg ggcgcggaag aagacttta 540
 ggagctacag actcaggga tcaaacttga aggcaccatt gccctgactc gatatggggg 600
 ttagggcggt ggggccaagg ctgtgaacgc tgccaagcac ggggtagctg ggggtgctgg 660
 gtacacagac cctgccgaca tcaacgatgg gctgagctca ccgacgaaa cctttcccaa 720
 ctcttggtac ctgccccct caggagtggg gcgaggctcc tactacgagt attttgggga 780
 ccctctgact ccctaccttc cagccgtccc ctcttccttc cgcgtggacc ttgccaatgt 840
 ctccggattt cccccaattc ctacacagcc cattggcttc caggatgcaa gagacctgct 900
 ctgtaacctc aacggaactt tggccccagc cacctggcag ggagcactgg gctgccacta 960
 caggttgggt cccggcttcc ggctgacgg agacttccca gcagacagcc aggtgaatgt 1020
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 ggctgtggag cctgatcgt acgtgctgta tgggaaccac cgagacagct ggggtgcacgg 1140
 ggctgtggac ccagcagtg gcaccgccgt cctcctggag ctctcccgtg tcctggggac 1200
 cctgctgaag aagggcacct ggcgtcctcg agatcaatc gtgtttgcga gctggggggc 1260
 tgaggagtgt gggctcattg gctccacgga attcacagaa gagttcttca acaagctgca 1320
 ggagcgacag gtggcctaca tcaacgtgga catctcggtg tttgccaacg ctacccttag 1380
 ggtgcagggg acgccccctg tccagagcgt cgtcttctct gcaaccaaag agatccgctc 1440
 accaggccct ggcgacctga gcatctacga caactggatc cggtaactta accgcagcag 1500

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ccccggtgtac ggccctgggtcc ccagcttggg ttctctgggt gctggcagcg actatgcacc 1560
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gacttcagcc aggatctacc ccacctacca cacagccttt gacacctttg actatgtgga 1680
caagttttttg gacccggtga ggagggagac aaggggcatc ctgagaccag gacaggagag 1740
gctgaagact gagccctggc cttgtcacct tgccgcaggg cttcagcagc catcaggctg 1800
tggcccggac agcggggagt gtgattctcc ggctcagtga cagcttcttc ctgcccctca 1860
aagtcagtga ctacagtga acactccgca gcttccctgca ggcagcccag caagatcttg 1920
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ttgaggcaga agctgcagcc ttgggccaac gcatatcaac actgcagaag ggcagccctg 2040
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accctagagc cttcccagag gaacgctact acagccatgt gctctgggca ccttcgcacg 2160
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ctggatctga agcttgggct gaggtccaga gacagctcag cattgtggtg acagccctgg 2280
aggggtgcggc agccaccctg aggcctgtgg ctgacctctg accccagccc tctttcttca 2340
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<210> 67
<211> 757
<212> PRT
<213> Homo sapiens

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<220>
<221> MOD_RES
<222> (100)
<223> variable amino acid

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<400> 67
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Leu Gly Leu Gly Ile Ile Leu Gly His Phe Ala Ile Pro Lys Lys Ala
      20              25              30

Asn Ser Leu Ala Pro Gln Asp Leu Asp Leu Glu Ile Leu Glu Thr Val
      35              40              45

Met Gly Gln Leu Asp Ala His Arg Ile Arg Glu Asn Leu Arg Glu Leu
      50              55              60

Ser Arg Glu Pro His Leu Ala Ser Ser Pro Arg Asp Glu Asp Leu Val
      65              70              75              80

Gln Leu Leu Leu Gln Arg Trp Lys Asp Pro Glu Ser Gly Leu Asp Ser
      85              90              95

Ala Glu Ala Xaa Thr Tyr Glu Val Leu Leu Ser Phe Pro Ser Gln Glu
      100             105             110

Gln Pro Asn Val Val Asp Ile Val Gly Pro Thr Gly Gly Ile Ile His
      115             120             125

Ser Cys His Arg Thr Glu Glu Asn Val Thr Gly Glu Gln Gly Gly Pro
      130             135             140

Asp Val Val Gln Pro Tyr Ala Ala Tyr Ala Pro Ser Gly Thr Pro Gln
      145             150             155             160

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Gly Leu Leu Val Tyr Ala Asn Arg Gly Ala Glu Glu Asp Phe Lys Glu
 165 170 175
 Leu Gln Thr Gln Gly Ile Lys Leu Glu Gly Thr Ile Ala Leu Thr Arg
 180 185 190
 Tyr Gly Gly Val Gly Arg Gly Ala Lys Ala Val Asn Ala Ala Lys His
 195 200 205
 Gly Val Ala Gly Val Leu Val Tyr Thr Asp Pro Ala Asp Ile Asn Asp
 210 215 220
 Gly Leu Ser Ser Pro Asp Glu Thr Phe Pro Asn Ser Trp Tyr Leu Pro
 225 230 235 240
 Pro Ser Gly Val Glu Arg Gly Ser Tyr Tyr Glu Tyr Phe Gly Asp Pro
 245 250 255
 Leu Thr Pro Tyr Leu Pro Ala Val Pro Ser Ser Phe Arg Val Asp Leu
 260 265 270
 Ala Asn Val Ser Gly Phe Pro Pro Ile Pro Thr Gln Pro Ile Gly Phe
 275 280 285
 Gln Asp Ala Arg Asp Leu Leu Cys Asn Leu Asn Gly Thr Leu Ala Pro
 290 295 300
 Ala Thr Trp Gln Gly Ala Leu Gly Cys His Tyr Arg Leu Gly Pro Gly
 305 310 315 320
 Phe Arg Pro Asp Gly Asp Phe Pro Ala Asp Ser Gln Val Asn Val Ser
 325 330 335
 Val Tyr Asn Arg Leu Glu Leu Arg Asn Ser Ser Asn Val Leu Gly Ile
 340 345 350
 Ile Arg Gly Ala Val Glu Pro Asp Arg Tyr Val Leu Tyr Gly Asn His
 355 360 365
 Arg Asp Ser Trp Val His Gly Ala Val Asp Pro Ser Ser Gly Thr Ala
 370 375 380
 Val Leu Leu Glu Leu Ser Arg Val Leu Gly Thr Leu Leu Lys Lys Gly
 385 390 395 400
 Thr Trp Arg Pro Arg Arg Ser Ile Val Phe Ala Ser Trp Gly Ala Glu
 405 410 415
 Glu Phe Gly Leu Ile Gly Ser Thr Glu Phe Thr Glu Glu Phe Phe Asn
 420 425 430
 Lys Leu Gln Glu Arg Thr Val Ala Tyr Ile Asn Val Asp Ile Ser Val
 435 440 445
 Phe Ala Asn Ala Thr Leu Arg Val Gln Gly Thr Pro Pro Val Gln Ser
 450 455 460

Val	Val	Phe	Ser	Ala	Thr	Lys	Glu	Ile	Arg	Ser	Pro	Gly	Pro	Gly	Asp	465	470	475	480
Leu	Ser	Ile	Tyr	Asp	Asn	Trp	Ile	Arg	Tyr	Phe	Asn	Arg	Ser	Ser	Pro	485	490	495	
Val	Tyr	Gly	Leu	Val	Pro	Ser	Leu	Gly	Ser	Leu	Gly	Ala	Gly	Ser	Asp	500	505	510	
Tyr	Ala	Pro	Phe	Val	His	Phe	Leu	Gly	Ile	Ser	Ser	Met	Asp	Ile	Ala	515	520	525	
Tyr	Thr	Tyr	Asp	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Ile	Tyr	Pro	Thr	Tyr	530	535	540	
His	Thr	Ala	Phe	Asp	Thr	Phe	Asp	Tyr	Val	Asp	Lys	Phe	Leu	Asp	Pro	545	550	555	560
Gly	Glu	Glu	Gly	Asp	Lys	Gly	His	Pro	Glu	Thr	Arg	Thr	Gly	Glu	Ala	565	570	575	
Glu	Asp	Phe	Ser	Ser	His	Gln	Ala	Val	Ala	Arg	Thr	Ala	Gly	Ser	Val	580	585	590	
Ile	Leu	Arg	Leu	Ser	Asp	Ser	Phe	Phe	Leu	Pro	Leu	Lys	Val	Ser	Asp	595	600	605	
Tyr	Ser	Glu	Thr	Leu	Arg	Ser	Phe	Leu	Gln	Ala	Ala	Gln	Gln	Asp	Leu	610	615	620	
Gly	Ala	Leu	Leu	Glu	Gln	His	Ser	Ile	Ser	Leu	Gly	Pro	Leu	Val	Thr	625	630	635	640
Ala	Val	Glu	Lys	Phe	Glu	Ala	Glu	Ala	Ala	Ala	Leu	Gly	Gln	Arg	Ile	645	650	655	
Ser	Thr	Leu	Gln	Lys	Gly	Ser	Pro	Asp	Pro	Leu	Gln	Val	Arg	Met	Leu	660	665	670	
Asn	Asp	Gln	Leu	Met	Leu	Leu	Glu	Arg	Thr	Phe	Leu	Asn	Pro	Arg	Ala	675	680	685	
Phe	Pro	Glu	Glu	Arg	Tyr	Tyr	Ser	His	Val	Leu	Trp	Ala	Pro	Ser	His	690	695	700	
Gly	Leu	Arg	Ser	His	Ile	Pro	Gly	Leu	Ser	Asn	Ala	Cys	Ser	Arg	Ala	705	710	715	720
Arg	Asp	Thr	Ala	Ser	Gly	Ser	Glu	Ala	Trp	Ala	Glu	Val	Gln	Arg	Gln	725	730	735	
Leu	Ser	Ile	Val	Val	Thr	Ala	Leu	Glu	Gly	Ala	Ala	Ala	Thr	Leu	Arg	740	745	750	
Pro	Val	Ala	Asp	Leu												755			

<210> 68
 <211> 2394
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (315)
 <223> a, c, g, t, unknown or other

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ggccccccag gacctggacc tggagatcct ggagaccgtc atggggcagc tggatgcccc 180
caggatcccg gagaacctca gagaactctc cagggagcca cacctggcct ccagccctcg 240
ggatgaggac ctggtgcagc tgctgctgca gcgctggaag gaccagagt caggcctgga 300
ctcgcccgag gcctncacgt acgaagtgtc gctgtccttc cctagccagg agcagcccaa 360
cgtcgtggac atcgtgggcc ccactggggg catcatccac tcctgccacc ggactgagga 420
gaacgtgacc ggggagcaag gggggccaga tgtggtacaa ccctatgctg cctatgctcc 480
ttctggaacc ccacagggcc tcctcgtcta tgccaaccgg ggcgcggaag aagactttaa 540
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tgtaggcgct ggggccaagg ctgtgaacgc tgccaagcac ggggtagctg ggggtgctggt 660
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ggtgcagggg acgccccctg tcagagcgt cgtcttctct gcaaccaaag agatccgctc 1440
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cccgtgttac ggcctggtcc ccagcttggg ttctctgggt gctggcagcg actatgcacc 1560
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gacttcagcc aggatctacc ccacctacca cacagccttt gacacctttg actatgtgga 1680
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gattctccgg ctcagtgaca gcttcttctt gcccctcaa gtcagtgact acagtgaag 1800
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gagccactgc ttgttcttca cagggggcct ctggtgactg cagtggagaa gtttgaggca 1980
gaagctgcag ccttggggcca acgcatatca acactgcaga agggcagccc tgacccccctg 2040
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gcagccaccc tgaggcctgt ggctgacctc tgacccagc cctctttctt cagccctccc 2340
tttactccgg tgctttatat ttacaaagtg ctttgtgttt tttaaaagtc tttt 2394
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<210> 69
 <211> 757
 <212> PRT
 <213> Homo sapiens

<220>

<221> MOD_RES

<222> (100)

<223> variable amino acid

<400> 69

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Leu Gly Leu Gly Ile Ile Leu Gly His Phe Ala Ile Pro Lys Lys Ala
 20 25 30

Asn Ser Leu Ala Pro Gln Asp Leu Asp Leu Glu Ile Leu Glu Thr Val
 35 40 45

Met Gly Gln Leu Asp Ala His Arg Ile Arg Glu Asn Leu Arg Glu Leu
 50 55 60

Ser Arg Glu Pro His Leu Ala Ser Ser Pro Arg Asp Glu Asp Leu Val
 65 70 75 80

Gln Leu Leu Leu Gln Arg Trp Lys Asp Pro Glu Ser Gly Leu Asp Ser
 85 90 95

Ala Glu Ala Xaa Thr Tyr Glu Val Leu Leu Ser Phe Pro Ser Gln Glu
 100 105 110

Gln Pro Asn Val Val Asp Ile Val Gly Pro Thr Gly Gly Ile Ile His
 115 120 125

Ser Cys His Arg Thr Glu Glu Asn Val Thr Gly Glu Gln Gly Gly Pro
 130 135 140

Asp Val Val Gln Pro Tyr Ala Ala Tyr Ala Pro Ser Gly Thr Pro Gln
 145 150 155 160

Gly Leu Leu Val Tyr Ala Asn Arg Gly Ala Glu Glu Asp Phe Lys Glu
 165 170 175

Leu Gln Thr Gln Gly Ile Lys Leu Glu Gly Thr Ile Ala Leu Thr Arg
 180 185 190

Tyr Gly Gly Val Gly Arg Gly Ala Lys Ala Val Asn Ala Ala Lys His
 195 200 205

Gly Val Ala Gly Val Leu Val Tyr Thr Asp Pro Ala Asp Ile Asn Asp
 210 215 220

Gly Leu Ser Ser Pro Asp Glu Thr Phe Pro Asn Ser Trp Tyr Leu Pro
 225 230 235 240

Pro Ser Gly Val Glu Arg Gly Ser Tyr Tyr Glu Tyr Phe Gly Asp Pro
 245 250 255

Leu Thr Pro Tyr Leu Pro Ala Val Pro Ser Ser Phe Arg Val Asp Leu
 260 265 270

Ala Asn Val Ser Gly Phe Pro Pro Ile Pro Thr Gln Pro Ile Gly Phe
 275 280 285
 Gln Asp Ala Arg Asp Leu Leu Cys Asn Leu Asn Gly Thr Leu Ala Pro
 290 295 300
 Ala Thr Trp Gln Gly Ala Leu Gly Cys His Tyr Arg Leu Gly Pro Gly
 305 310 315 320
 Phe Arg Pro Asp Gly Asp Phe Pro Ala Asp Ser Gln Val Asn Val Ser
 325 330 335
 Val Tyr Asn Arg Leu Glu Leu Arg Asn Ser Ser Asn Val Leu Gly Ile
 340 345 350
 Ile Arg Gly Ala Val Glu Pro Asp Arg Tyr Val Leu Tyr Gly Asn His
 355 360 365
 Arg Asp Ser Trp Val His Gly Ala Val Asp Pro Ser Ser Gly Thr Ala
 370 375 380
 Val Leu Leu Glu Leu Ser Arg Val Leu Gly Thr Leu Leu Lys Lys Gly
 385 390 395 400
 Thr Trp Arg Pro Arg Arg Ser Ile Val Phe Ala Ser Trp Gly Ala Glu
 405 410 415
 Glu Phe Gly Leu Ile Gly Ser Thr Glu Phe Thr Glu Glu Phe Phe Asn
 420 425 430
 Lys Leu Gln Glu Arg Thr Val Ala Tyr Ile Asn Val Asp Ile Ser Val
 435 440 445
 Phe Ala Asn Ala Thr Leu Arg Val Gln Gly Thr Pro Pro Val Gln Ser
 450 455 460
 Val Val Phe Ser Ala Thr Lys Glu Ile Arg Ser Pro Gly Pro Gly Asp
 465 470 475 480
 Leu Ser Ile Tyr Asp Asn Trp Ile Arg Tyr Phe Asn Arg Ser Ser Pro
 485 490 495
 Val Tyr Gly Leu Val Pro Ser Leu Gly Ser Leu Gly Ala Gly Ser Asp
 500 505 510
 Tyr Ala Pro Phe Val His Phe Leu Gly Ile Ser Ser Met Asp Ile Ala
 515 520 525
 Tyr Thr Tyr Asp Arg Ser Lys Thr Ser Ala Arg Ile Tyr Pro Thr Tyr
 530 535 540
 His Thr Ala Phe Asp Thr Phe Asp Tyr Val Asp Lys Phe Leu Asp Pro
 545 550 555 560
 Gly Phe Ser Ser His Gln Ala Val Ala Arg Thr Ala Gly Ser Val Ile
 565 570 575

Leu Arg Leu Ser Asp Ser Phe Phe Leu Pro Leu Lys Val Ser Asp Tyr
 580 585 590
 Ser Glu Thr Leu Arg Ser Phe Leu Gln Ala Ala Gln Gln Asp Leu Gly
 595 600 605
 Ala Leu Leu Glu Gln His Ser Ile Ser Leu Gly Met His Ser Pro Asp
 610 615 620
 Pro Glu Val Trp Gly Ala Leu His Pro His Asp Gly Pro Leu Val Thr
 625 630 635 640
 Ala Val Glu Lys Phe Glu Ala Glu Ala Ala Ala Leu Gly Gln Arg Ile
 645 650 655
 Ser Thr Leu Gln Lys Gly Ser Pro Asp Pro Leu Gln Val Arg Met Leu
 660 665 670
 Asn Asp Gln Leu Met Leu Leu Glu Arg Thr Phe Leu Asn Pro Arg Ala
 675 680 685
 Phe Pro Glu Glu Arg Tyr Tyr Ser His Val Leu Trp Ala Pro Ser His
 690 695 700
 Gly Leu Arg Ser His Ile Pro Gly Leu Ser Asn Ala Cys Ser Arg Ala
 705 710 715 720
 Arg Asp Thr Ala Ser Gly Ser Glu Ala Trp Ala Glu Val Gln Arg Gln
 725 730 735
 Leu Ser Ile Val Val Thr Ala Leu Glu Gly Ala Ala Ala Thr Leu Arg
 740 745 750
 Pro Val Ala Asp Leu
 755